

FIGURE 1

1 agcctttact ttctttcaa cttttcatcc cgatacttt tgtaatagt tttttcatt
 61 aataatacaa gtcctgatit tgcaagaata atcctttta gataaaaata tctatgtcaa
 121 taataacatg taaccactta cattaaaaaa ggagtgttat catgttatat ccaatcaata
 181 cagaaacccg aggagttttt gattnaatg gggcttgaa ttttaattt gattacggca
 241 aaggactgga agaaaagtgg tatgaatcaa aactgacaga taccatatca atggctgtac
 301 cttccctcta taatgatatc ggtgttacga agggaaattcg aaaccatatc ggctatgtat
 361 ggtacgagcg tgaatttacc gttcctgttt attttaaaaga tcagcgcattc gtccctgcgtt
 421 ttggttcaac aacacataag gctattgtat acgttaacgg agaacttagt gttgaacaca
 481 aaggcggctt cttaacggttt gaggcagaaa taaaacaacag cttaagagac ggaatgaatc
 541 gtgtacagt agcggtttagt aatatttttag atgattctac gtcctttagt gggctatata
 601 gtgaaagaca tgaagaagggtt tggggaaaag tgattcgtaa taaacctaattt tttgacttct
 661 ttaactatgc agggtttacat cgtcctgttaa aaatttataac aaccctttt acctatgtt
 721 aggatataatc ggttgttaacc gattnnaacg gtccaaacggg aacagttacg tatacagg
 781 attttcagggtt taaggcagaa accgtttaagg tttagttagt tgatgaaagaa gggaaagg
 841 ttgcttcaac tgaaggcctc tctggtaatg ttggatcc taaacgttac ctttggaaac
 901 cttaaaatatac ctatctctat caaaattaaatg ttgagtttagt aaatgttggt ctaactatt
 961 atgtatacga agagccattt ggagttcgaa ccgttgaagt aaacgcacggg aaattcccta
 1021 ttaataacaa accatttat tttaaagggt tccggaaaaca cgaggatactt ccaataatg
 1081 gaaagggtt taatgaaagg tcaaattgtaa ttggatcc tattttgaaa tggatcggrg
 1141 cyaattccctt tcggacggcg cactatctt atctgttgg actgtatgcgg ctggcagat
 1201 gtgtacgggtt agtcgttata gatgaaaccc cagcgttgg tggatcc ttttgcgtt
 1261 caacgactgg tttggcgaa ggttccagaga gagttgttac ttggaaaaaa atccggaccc
 1321 ttgttacatca tcaagatgtt ctggatcc tggatcc tggatcc ttttgcgtt
 1381 ttgttacatgtt gtcgttggca aatgaaaggcg ctacggaaaga agaaggcgct tatgttac
 1441 ttaagccattt agttgttggca acgaaagsat tagatccaca aaaacgcctt gttaccatt
 1501 ttttgcgtt aatggcgacca ccagaaacag ataaatgtggc ggaggtaattt gatgttgcgtt
 1561 cattgttacatcg atacaacggc tggatcc ttttgcgtt aatggatcc gcgaaaggcc
 1621 accttcgttca ggaatttccat gctgttggaaata aacgttgcgtt agggaaaaccc ataaatgtt
 1681 cagagttatgg ggcgttgcattt gtagttgggtt ttttgcgtt ttttgcgtt
 1741 aagagttatca ggttggatata taccatggaa atcatgttgg attttgcgtt ttttgcgtt
 1801 ttgttggcgaa gcaggccgtt aattttgcgtt accttgcgtt aagccagggt gtcgttgcgtt
 1861 ttcaaggtaa caaaaaaaaa gtttccatcg gctgttgcgtt aaccaaaatca gcaacatcg
 1921 ttttccgcgtt acgttggatca aacatccccgg attttgcgtt taaaatca taaaatgtt
 1981 gtttccatcg aaggaggccgg cttttttaca tggatccaa gtttgcgtt taaaatcc
 2041 ttttgcgtt ttttgcgtt ttttgcgtt ttttgcgtt ttttgcgtt ttttgcgtt

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GLUCURONIDASE GENES, GENE
PRODUCTS AND USES THEREOF
Inventor(s): JEFFERSON ET AL.
DOCKET NO.: 076518-0150

FIGURE 2

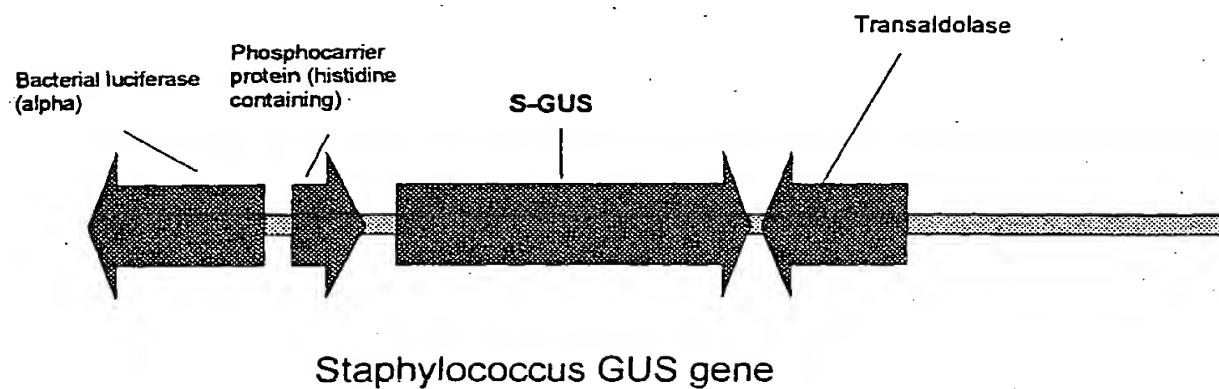


FIGURE 3A

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A*Staphylococcus* β -glucuronidase

1 MLYPINTETR GVFDLNGVWN FKLDYGKGLE EKWYESKLTD TISMAVPSSY
 51 NDIGVTKEIR NHIGYVWYER EFTVPAYLKD QRIVLRFGSA THKAIVYVNG
 101 ELVVEHKGGF LPFEAEINNS LRDGMNRVTV AVDNILDDST LPVGLYSERH
 151 EEGLGKVRN KPNFDFFNYA GLHRPVKIYT TPFTYVEDIS VVTDENGPTG
 201 TVTYTVDFQG KAETVKVSVV DEEGKVVAST EGLSGNVEIP NVILWEPLNT
 251 YLYQIKVELV NDGLTIDVYE EPFGVRTVEV NDGKFLINNK PFYFKGFGKH
 301 EDTPINGRGF NEASNVMDFN ILKWIGANSF RTAHYPYSEE LMRLADREGL
 351 VVIDETPAVG VHLMFMATTG LGEGSERVST WEKIRTFEHH QDVLRELVS
 401 DKNHPSVVMW SIANEAATEE EGAYEYFKPL VELTKELDPQ KRPVTIVLFV
 451 MATPETDKVA ELIDVIALNR YNGWYFDGGD LEAAKVHLRQ EFHAWNKRCP
 501 GKPIMITEYG ADTVAGFHDI DPVMFTEEYQ VEYYQANHVV FDEFENFVG
 551 QAWNFAADFAT SQGVMRVQGN KKGVFTRDRK PKLAHVFR RWTNIPDFGY
 601 KN

B*Enterobacter/Salmonella* β -glucuronidase

1 GKLSPTPTAY IQDVTVXTDV LENTEQATVL GNVGADGDIR VELRDGQQQI
 51 VAQGLGATGI FELDNPHLWE PGEGLYELR VTCEANGECD EYPVRVGIRS
 101 ITXKGSEQFLI NHKPFYLTGF GRHEDADFRG KGFDPVLMVH DHALMNWIGA
 151 NSYRTSHYPY AEKMLDWAD EHVIVVINETA AGGFNTLSLG ITFDAGERPK
 201 ELYSEEAAING ETSQQAHLQA IKELIARDKN HPSVVCWSIA NEPDTRPNGA
 251 REYFAPLAKA TRELDPTRPI TCVNVMFCDA ESDTITDLFD VVCLNRYYGW
 301 YVQSGDLEKA EQMLEQELLA WQSKLHRPII ITEYGVDTLA GMPSVYPDMW
 351 SEKYQWKWLE MYHRVFDRGS VC

C*Staphylococcus homini* β -D-glucuronidase

1 GLSGNVEIPN VILWEPLNTY LYQIKVELVN DGLTIDVYEE PFGVRTVEVN
 51 DGKFLINNK P FYFKGFGKHE DTPINGRGFN EASNVMDFNI LKWIGANSFR
 101 TAHYPYSEEL MRLADREGLV VIDETPAVGV HLNFMATTGL GEGSERVSTW
 151 EKIRTFEHHQ DVLRELVS RD KNHPSVVMWS IANEAATEEE GAYEYFKPLG
 201 GAAKELDPXK RPVTIVLFV M ATPETDKVAE LIDVIALNRY NGWYFDGGDL
 251 EAAKVHLRQE FHAWNKRCPG KPIMITEYGA DTAGFHDID PVMFTEEYQV
 301 EYYQANHVVF DEFENFVG EQ AWNFADFATS QGVMRVQGNK KGKVFTRDRKP
 351 XLAHVFRER RTNIPDFGYK NASHHH

FIGURE 3B**09/936759****D***Staphylococcus warneri* β -D-glucuronidase

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1  LXLLHPITTG TRGGFALYGX XNLMLDYGXG LTDWTXSSL TELSRLVVLS
51  WTTHXLITGEX PAISILWPNS ELTVSXLYXG SLXSSSXLCs SLTXHVVICQ
101  XVTLXVDRHTG LIXXFEMST TCCXXDELVT GTLAXILYHX ILPHGLYRKR
151  HEXGLGKCNF YXLHFAFFXY AXLXRTVXMY XNLVRXQDIX VVTXXHXXXX
201  TVEQCVXXNX KIXSVKITIL DENDHAIXES EGAKGNVTIQ NPILWQPLHA
251  YLYNMKVELL NDNECVDVYT ERFGIRSVEV KDGQFLINDK PFYFKGFGKH
301  EDTYXNGRGL NESANVMDIN LMKWIGANSF RTSHYPYSEE MMRLADEQGI
351  VVIDETTXVG IHLNFMXTLG GSXAHDWTXE FDTLEFHKEV IXDLIXRDKN
401  HAWVVMWXFG NEXGXNKGGA KAXFEPFVNl AGEKDXXXXP VTIVTILXAX
451  RNVCEVXDLV DVVCLXXXG WYXQSGDLEG AKXALDKEXX EWWKCKQXNKP
501  XMFTEYGVDX VVGLXXXPDK MXPEEYKMXF YKGYXXIMDK

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E*Thermotoga maritima* β -glucuronidase

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1  MVRPQRNKKR FILILNGVWN LEVTSKDRPI AVPGSWNEQY QDLCYEEGPF
51  TYKTTTFYVPK XLSQKHIRLY FAAVNTDCEV FLNGEKVGEN HIEYLPFEVD
101  VTGKVKGEn ELRVVVENRL KVGGFP SKVP DSGTHTVGFF GSFPPANFDF
151  FPYGGIIRPV LIEFTDHARI LDIWVDTSES EPEKKLGKVJK VKIEVSEEAV
201  GQEMTIKLGE EEEKKIRTSNR FVEGEFILEN ARFWSLEDPY LYPLKVELEK
251  DEYTLDIGIR TISWDEKRLY LNGKPVFLKG FGKHEEFPVL GQGTFYPLMI
301  KDFNLLKWIN ANSFRTSHYP YSEEWLDLAD RLGLILVIDEA PHVGITRYHY
351  NPETQKIAED NIRRMIDRHk NHPSVIMWSV ANEPESNHPD AEGFFKALYE
401  TANEMDRTRP VVMVSMMDP DERTRDVALK YFDIVCVNRY YGWYIYQGRI
451  EEGLQALEKD IEELYARHRK PIFVTEFGAD AIAGIHYDPP QMFSEEVQAE
501  LVEKTIRLLL KKDIYIIGTHV WAFADF KTPQ NVRRPILNHK GVFRDRQPK
551  LVAHVLRRIW SEV

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FIGURE 4A**09/936759*****Staphylococcus* β-glucuronidase**

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MetLeuTyrProIleAsnThrGluThrArgGlyValPheAspLeuAsnG1
1 ATGTTATATCCAATCAATACAGAAACCGAGGAGTTTGATTAAATGG

yValTrpAsnPheLysLeuAspTyrGlyLysGlyLeuGluGluLysTrpT
51 GGTCTGGAATTTAAATTAGATTACGGCAAAGGACTGGAAGAAAAGTGGT

yrGluSerLysLeuThrAspThrIleSerMetAlaValProSerSerTyr
101 ATGAATCAAAACTGACAGATACCATATCAATGGCTGTACCTCCTCCTAT

AsnAspIleGlyValThrLysGluIleArgAsnHisIleGlyTyrValTr
151 AATGATATCGGTGTTACGAAGGAAATCGAAACCATACTGGCTATGTATG

pTyrGluArgGluPheThrValProAlaTyrLeuLysAspGlnArgIleV
201 GTACGAGCGTGAATTTCACGTTCTGCTTATTAAAAGATCAGCGCATCG

alLeuArgPheGlySerAlaThrHisLysAlaIleValTyrValAsnGly
251 TCCTGCGTTTGGTTCAAGAACACATAAGGCTATTGTATACGTTAACCGA

GluLeuValValGluHisLysGlyGlyPheLeuProPheGluAlaGluI1
301 GAACTAGTAGTTGAACACAAAGGCGGCTTACCGTTGAGGCAGAAAT

eAsnAsnSerLeuArgAspGlyMetAsnArgValThrValAlaValAspA
351 AAACAACAGCTTAAGAGACCGGAATGAATCGTAAACAGTAGCGGTTGATA

snIleLeuAspAspSerThrLeuProValGlyLeuTyrSerGluArgHis
401 ATATTTAGATGATTCTACGCTCCCAGTTGGGCTATATAGTGAAAGACAT

GluGluGlyLeuGlyLysValIleArgAsnLysProAsnPheAspPhePh
451 GAAGAAGGTTGGGAAAAGTGATTGTAATAAACCTAATTTGACTTCTT

eAsnTyrAlaGlyLeuHisArgProValLysIleTyrThrThrProPheT
501 TAACTATGCAGGCTTACATCGTCCTGTAAAAATTATACAACCCCTTTA

hrTyrValGluAspIleSerValValThrAspPheAsnGlyProThrGly
551 CCTATGTTGAGGATATACGGTTGTAACCGATTAAACGGTCCAACGGGA

ThrValThrTyrThrValAspPheGlnGlyLysAlaGluThrValLysVa
601 ACAGTTACGTATACAGTTGATTTCAGGGTAAGGCAGAAACCGTAAAGGT

1SerValValAspGluGluGlyLysValValAlaSerThrGluGlyLeuS
651 TAGTGTAGTTGATGAAGAAGGGAAAGTTGCTTCAACTGAAGGCCTCT

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FIGURE 4B

701 erGlyAsnValGluIleProAsnValIleLeuTrpGluProLeuAsnThr
 CTGGTAATGTTGAGATTCTAACGTTATCCTTGGAACCTTAAATACC
 TyrLeuTyrGlnIleLysValGluLeuValAsnAspGlyLeuThrIleAs
 751 TATCTCTATCAAATTAAAGTTGAGTTAGTAAATGATGGTCTAACTATTGA
 pValTyrGluGluProPheGlyValArgThrValGluValAsnAspGlyL
 801 TGTATACGAAGAGCCATTGGAGTCGAACCGTTGAAGTAAACGACGGGA
 ysPheLeuIleAsnAsnLysProPheTyrPheLysGlyPheGlyLysHis
 851 AATTCCCTCATTAATAACAAACCATTATTTAAAGGGTTCGGAAAACAC
 GluAspThrProIleAsnGlyArgGlyPheAsnGluAlaSerAsnValMe
 901 GAGGATACTCCAATAATGGAAGAGGCTTAATGAAGCATCAAATGTAAT
 tAspPheAsnIleLeuLysTrpIleGlyAlaAsnSerPheArgThrAlaH
 951 GGATTAAATATTGAAATGGATCGGTGCGAATTCTTCGGACGGCGC
 isTyrProTyrSerGluGluLeuMetArgLeuAlaAspArgGluGlyLeu
 1001 ACTATCCTTATTCTGAAGAACTGATGCGGCTCGCAGATCGTGAAGGGTTA
 ValValIleAspGluThrProAlaValGlyValHisLeuAsnPheMetAl
 1051 GTCGTCATAGATGAAACCCAGCAGTTGGTGTCAATTGAACTTTATGGC
 aThrThrGlyLeuGlyGluGlySerGluArgValSerThrTrpGluLysI
 1101 AACGACTGGTTGGCGAAGGTTCAGAGAGAGTGAGTACTTGGGAAAAAA
 leArgThrPheGluHisHisGlnAspValLeuArgGluLeuValSerArg
 1151 TCCGGACCTTGAAACATCATCAAGATGTACTGAGAGAGCTGGTTCTCGT
 AspLysAsnHisProSerValValMetTrpSerIleAlaAsnGluAlaAl
 1201 GATAAAAACCACCCCTCTGTTGTATGTGGTCATTGCAAATGAAGCGGC
 aThrGluGluGluGlyAlaTyrGluTyrPheLysProLeuValGluLeuT
 1251 TACGGAAGAAGAAGGCGTTATGAATACTTTAAGCCATTAGTTGAATTAA
 hrLysGluLeuAspProGlnLysArgProValThrIleValLeuPheVal
 1301 CGAAAGAATTAGATCCACAAAACGCCAGTTACCAATTGTTTGTTCGTA
 MetAlaThrProGluThrAspLysValAlaGluLeuIleAspValIleAl
 1351 ATGGCGACACCAGAAACAGATAAAAGTGGCGGAGTTAATTGATGTGATTGC
 aLeuAsnArgTyrAsnGlyTrpTyrPheAspGlyGlyAspLeuGluAlaA
 1401 ATTGAATCGATACAACGGCTGGTATTGATGGGGGTGATCTTGAAGCCG

FIGURE 4C

1aLysValHisLeuArgGlnGluPheHisAlaTrpAsnLysArgCysPro
1451 CGAAAGTCCACCTTCGTCAGGAATTCATGCGTGGAAATAACGCTGTCCA

GlyLysProIleMetIleThrGluTyrGlyAlaAspThrValAlaGlyPh
1501 GGAAAACCTATAATGATAAACAGAGTATGGGGCTGATAACCGTAGCTGGTTT

eHisAspIleAspProValMetPheThrGluGluTyrGlnValGluTyrT
1551 TCATGATATTGATCCGGTTATGTTACAGAAGAGTATCAGGTTGAATATT

yrGlnAlaAsnHisValValPheAspGluPheGluAsnPheValGlyGlu
1601 ACCAAGCAAATCATGTAGTATTGATGAATTGAGAACTTGTTGGCGAG

GlnAlaTrpAsnPheAlaAspPheAlaThrSerGlnGlyValMetArgVa
1651 CAGGCCTGGAATTTCAGACTTGCTACAAGCCAGGGTGTATGCGTGT

1GlnGlyAsnLysLysGlyValPheThrArgAspArgLysProLysLeuA
1701 TCAAGGTAACAAAAAGGTGTTTACACCGCACCGCAAACCAAAATTAG

1aAlaHisValPheArgGluArgTrpThrAsnIleProAspPheGlyTyr
1751 CAGCACATGTTTCCCGCGAACGTTGGACAAACATCCCGGATTCGGTTAT

LysAsn
1801 AAAAAT

FIGURE 4D***Enterobacter/Salmonella* β -glucuronidase gene**

CATTGGGGAACTTCCCCCACACCTACTGCGTATATTCA	GATGTTACG 50
GGTTNTTACTGATGTTTGAAAATACTGAACAGGCGACCGTA	ACTGGGGA 100
ATGTGGGGCTGATGGTGAATTGGGTTGAGCTTCGCGATGGGCAGCAA	150
CAAATAGGGCACAAGGGCTGGGGCACAGGTATATTGA	ACTGGATAA 200
TCCTCATTTGGAACCCAGGTGAAGGGTATTGTACGAGCTGCGGGTTA	250
CCTGCGAAGCCAATGGTGAGTGTGACGAATATCCAGTACGTGTCGGTATC	300
CGTTCCATTACGGNTAAGGGTGAGCAGTTTGATTAACCACAAACCGTT	350
TTATTTAACCGGTTTGGTCGACATGAAGATGCAGATTTCGCGGCAA	400
GGTTTCGACCCGGGTGTTGATGGTTCACGACCACCGCGTGTGATGA	ACTGG 450
TTGGGCTAACTCCTATCGCACGTCCCAC	TACCGCGGAAAAGATGC 500
TCGATTGGCTGATGAGCACGTATCGTAGTGATTAATGAAACCGCGGCGG	550
GTGGCTTAAACACTTATCGTTGGGAATCACTTTGACGCAGGCGAAAGA	600
CCTAAAGAACTTCTACAGCGAAGAGGGGATTAATGGCGAGACTTCAGCAG	650
GCTCACTTGCAGGCTATAAAAGAGCTTATTGCCCGGATAAAACCATCC	700
AAGTGTAGTGTGGAGTATTGCCAATGAGCCGACACCCGTCCAATGG	750
AGCCAGAGAGTACTTTCGCCTTAGCTAAGGCCACTCGTGA	ACTGGATC 800
CGACACGTCCGATTACCTGCGTAAACGTGATGTTCTGCGATGCCGAAAGC	850
GACACCATCACCGACCTGTCGACGTGGTTGTCTGAATCGCTATTACGG	900
CTGGTATGTCAATCAGGTGATTGGAAAAAGCAGAACAGATGCTGGAGC	950
AAGAACTGCTGGCCTGGCAGTCAAAACATCGCCAATTATTACG	1000
GAATACGGTGTGATA	CGCTGGCAGGAATGCCCTCGGTTATCCGACAT 1050
GTCGGAGTAAAAGTACCA	CGTGAATGGCTTGAAATGTATCACC GTGCTT 1100
TGACCGGGGGAGCGTTGCAAGCGCNAAGCTTAGTTAACACCGGNGGTAC	1150
CGATCACCGTNAGGCCNCCATGGNCATATGNGCTAGCNTGCGGCCG	1200

FIGURE 4E

CNATGCATTCTGCAGCGATCGCAGCTGAGTACACGAGCTCACCCGGAG 1250

TCGACAAGATCCAAGTACTACCCGGGNATACGTAACTAGTGCATGCTCGC 1300

GAAATATTAGGCCTTATCGAATTAAT 1328

Pseudomonas β -D-glucuronidase

CTTGCTGGACNACNGTTNAGGATTTTAGACACGNGGAGCTAAAGCTTGC 50
 TGACCNAACTATCACGCCGGNCGTGCANGCTTGGACCGCGACATTNCCTG 100
 ACANGNGAAANACTCCGCCATATCCATCTTGCTGGCCAACAGTGAGTT 150
 NACNGTNNCGNACNNNTNGANGGATCAGTGNATCGAGCTCCNTTNANNTT 200
 CTNCGCTAACATAACATGTNGCATATGTCAATNAATNACGCTGGNCGTGG 250
 ANCNCACCGGGCTNATTGNTGNNATTGAATTGNATGNCAACAACINTG 300
 NTGCACGNTGGNAAANAATTGCGTNACAGGGACTITGGCNCTTCCTAAA 350
 CCATNGCATCCTCCNATGGGCTGTACACGAATGNGCCCCAAAANGCN 400
 TTCAGAAAGGCAATTNTAACAGGCNGANNTTGACTTTTCAACTATG 450
 CAGNNCTGCACCGGACGCTGAAAATGTACANGACCCTGGTACGTNCNAC 500
 CAAGACATNNAAAGTNGTACCGACTCCATTGTNCTAACCGGGACTGTACC 550
 TATAATGCGGACTATCANGCAATGCATGACGTNGAANCACACACCAGG 600
 ATNAGGAAAACAANTGGTGGNANCNCACCANGCCATGATTGTCACGTTT 650
 GTTAGCNTNGANACNAATTNCTTNTAGCTTNTTANATNAGCCT 700
 NTTTANATTAGANTTCTNANTGAGACTGT 730

Salmonella β -glucuronidase

NCTCATGACCCNCCNNTTNTGTCAGTANCNTNTTGNNACTGCTGCANNNGA 50
 TCACNACNNGGANNCGGGGGGGTTCGNNCTCTATGGCNCNGGAACNNN 100
 ATGNTGGNCNACNGTTNANGACTGACAGACACGTGGAGCTAAAGCTTGCT 150

FIGURE 4F

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GCCGAACATCACTCAGNTCNTGNAAGTTGGACAACACATTNCCTGACAN	200
GNGAAAAGCCCGCCATATCCATACTGTGCTGGCCAACANTGAGTCACN	250
GTCGTCGNACTNTATGANGGATCACCTGTATCGANCTCCNTTNAATNTTCT	300
NCAGCTAACATAACTGTGNGCATATGTCAATGNATGACCTGGTCGGTGNA	350
NCACACCGGGCGTNATTGNTGNNATTGAAATTINATGTCAACAACTTGN	400
TGCANGNTGGAATGAATCTGGGGCCAGGGACTTGGCCANCTTCTNAA	450
CCATTGCGANCCTCCCCAGTGGCTTGACACNATTGNGCCCCAAAAAG	500
GCNTCAGATAGGCATTTGACAAGCTCCANNTAACTTTTCAACTATGC	550
NGNCCTGCACCGGACGCTGAAAAANGTACANGANCCTGTACGTTCCACC	600
AAGANATTIAAGGTGTACCCACNTCCATTTCCTAACNGGACTGTGACT	650
NATAAAGGNTGACCNTTCANGGACACATTGCAATGACCCTTNAACGGA	700
ANAACCCCCGGNTAAAGGAAAAACAAATTGGTTGGGNAGTCCANCAA	750
GGGCCAATTANTTGTNCNGGGGANTAAANCCCCNCCAATGATCTT	800
CGAAATTAAACAGCGCTCCGGCCACGTGCAATTCCGATATCGGAT	850
GAGGCCAGCGCNAAGCTTAGTTAACACCGGNGGTACCGATCACCGTNAG	900
GCGCCNCCCATGGNCATATGNGCTAGCNTGCGGCCNATGCATTCTGCA	950
GCGATCGCAGCTGAGTACACGAGCTACCCGGAGTCGACAAGATCAA	1000
GTACTACCCGGGNATACGTAACTAGTGCATGCTCGCGAAATATTIAGGCC	1050
TTATCGAATTAA	1063

Staphylococcus warneri β -glucuronidase

TANANCTTGTNTCTGCTGCACCNATCACGACAGGGACCCGGGGNGGTT	50
CGCGCTCTATGGCNCNGGAACCTAATGCTGGACTACGGTTNAGGACTGA	100
CAGACACGTGGACTNAAAGCTTGCTGACCGAACTATCACGACTGGTCGTG	150
CTAAGTTGGACCACACATNCCTGACAGGGAAANACCGCCATATCCAT	200

FIGURE 4G

CTTGTGGCCAACAGTGAGTTAACCGTGTGANCTTATGANGGATCAC 250
 TGNATTGAGCTCCNTCTTATGTTCTCGCTAACATANCATGTNGTCATA 300
 TGTCAATANGTGACNCTGGNCGTGGATCACACCCGGCTNATTGNTGNATT 350
 CGAATTATGTCAACAACCTGTTGCANGNTGGATGAATTGGTNACAGGGA 400
 CTTGGCCANCATCCTATACCATNGCATCCTCCCCATGGGCTTACCGA 450
 AAGGCCACGAAAANGGCCTCGGAAAAGNCAATTTCACNGGCTCCACTT 500
 TGCNTTTCAANTATGCNGANCTGNACCGGACGGTNANAATGTACANGA 550
 ACCTTGTACGTCNNCAAGACATTAGGTTGTGACCGNTTAGCATNAGCNG 600
 TNNTAAACAGTAGAACAAATGTGTGANCCNTAACTAAAAAATANACAGCGT 650
 TAAAATCACGATTCTGGATGAAAATGATCATGCAATANCCGAAAGCGAAG 700
 GCGCTAAAGGCAATGTAACATTCAAAATCCTATATTGTGGCACCTTTA 750
 CATGCCTATTTATACAATATGAAAGTAGAATTACTAACGATAATGAGTG 800
 TGTAGATGTTATACAGAACGTTCGGTATTCGATCTGTNGAAGTGAAGG 850
 ATGGACAGTTTTAATTAATGACAAACCATTTCATTCAAAGGTTCGGT 900
 AAACATGAAGATAACCTATTAAAATGGTCGAGGCTAACGAATCAGCCAA 950
 CGTCATGGACATCAACTTAATGAAATGGATAGGTGCTAATTCAATTAGAA 1000
 CCTCTCATTACCCATATTCAAGAACGTTAGCCTTACGAGATGAACAA 1050
 GGTATTGTAGTGATAGATGAGACAACANGTGTGGTACATCTTAATT 1100
 TATGGNNACCTTAGGTGGCTCCNTGCACATGATAACATGGAANGAATTG 1150
 AACACTCTCGAGTTCAAAAGAAGTCATANAAGACTTGATTGNGAGAGAC 1200
 AAGAATCATGCATGGTAGTCATGTGGTNATTGGCAATGAGCNAGGGTN 1250
 AAATAAAGGGGGTGCTAAAGCATNCNTTGAGCCATTGTTAATTAGCAG 1300
 GTGAAAAAGATNNTCGNNTNGCCAGTGACTATCGTTACTATATTANCT 1350
 GCNNANCAGAAATGTATGTGAAGTTAGTCGATGTGGTTGTCT 1400

FIGURE 4H

NNNNAGNNNTANGTTGGTATNCACAATCAGGTGATTAGAAGGTGCTA 1450
 AACNAGCATTAGATAAGGAGNTAGNCGAATGGTGGAAANGACAACNAAAT 1500
 AAGCCAATNATGTTACAGAGTATGGTGTGGATANNGTTAGGTTACA 1550
 NNCGATNCCTGATAAAATGCNNCCAGAACAGTATAAAATGAGNTTTATA 1600
 AAGGNTATNATAAAATTATGGATAAACGATCGCAGCTGAGTACACGAGCT 1650
 CACCCGGAGTCGACAAGATCCAAGTACTACCCGGGNATACGTAACTAG 1700
 TGCATGCTCGCAAATATTAGGCCTATCGAATTAAT 1739

Staphylococcus homini β -glucuronidase gene

TGTGGGNCTTGTCCTGNTCAGCTCCCCAACGGCTTGAAGTACTCGTA 50
 CGCGCCCTCTCCTCAGTCGCCCTCGTGGCATGCTCACATCAGA 100
 CGCTTGGATGGTTCTGTCACGAGACACCAGTTACGGAGAACGTCTTGA 150
 TGGTGCTAACGTCCGAATCTCTCCAGGTACTGACGCCGCTCGCTGCC 200
 TTCGCCGAGTCCC GTGGTGGCCATGAAGTTGAGGTGCACGCCAAGTCCG 250
 GAGTCTCGTCGATCACGACCAGACCCCTCGCGATCCGCAAGACGCATCAAC 300
 TCTTCAGAGTACGGATAGTGTGCGGTCCGGAAAGCTGTTGGCGCCGATCCA 350
 TTGAGGATATTGAAATCCATCACATTGCTCGCTCGTTAAAGCCACGGC 400
 CGTTGATAGGAGTGTCCCTCATGTTGCCAAAGCCCTGAAGTAGAACGGT 450
 TTGTTGTTGATGAGGAACCTGCCGTCGTTGACTTCACGGTCCGCACGCCG 500
 AACGGCTCTCATAGACATCGATGGTCAAGTCCC GTCGTTCACCAAGTCC 550
 ACTTTGATCTGGTAGAGATACTGTGTTCAAGTGGTCCCAGAGGATGACAT 600
 TCGGAATCTTCACGTTACCGCTCAAGCC 629

FIGURE 4I

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Thermotoga maritima β -glucuronidase

ATGGTAAGACCGCAACGAAACAAGAAGAGATT	50
AGTTTGAATCTTGAAGTAACCAGCAAAGACAGACCAATGCCGTCCTG	100
GAAAGCTGGAATGAGCAGTACCAAGGATCTGTGCTACGAAGAAGGACCC	150
ACCTACAAAACCACCTCTACGTTCCGAAGNAACTTCACAAAAACACAT	200
CAGACTTTACTTTGCTGCGGTGAAACACGGACTGCGAGGTCTCCTCAACG	250
GAGAGAAAGTGGGAGAGAATCACATTGAATACTTCCCTCGAAGTAGT	300
GTGACGGGAAAGTGAAATCCGGAGAGAACGAACTCAGGGTGGTTGA	350
GAACAGATTGAAAGTGGGAGGATTCCCTCGAAGGTTCCAGACAGCGGCA	400
CTCACACCGTGGATTGGAGTTGAAGTTCCACCTGCAAACCTCGACTTC	450
TTCCCCCTACGGTGGAAATCATAAGGCCTGTTCTGATAGAGTTCACAGACCA	500
CGCGAGGATACTCGACATCTGGGTGGACACGAGTGAGTCTGAACCGGAGA	550
AGAAACTTGGAAAAGTGAAGATAGAAGATCTCAGAAGAAGCGGTG	600
GGACAGGAGATGACGATCAAACCTGGAGAGGAAGAGAAAAAGATTAGAAC	650
ATCCAACAGATTGTCGAAGGGAGTTCATCCTCGAAAACGCCAGGTCT	700
GGAGCCTCGAAGATCCATATCTTATCCTCTCAAGGTGAACTTGAAGGAA	750
GACGAGTACACTCTGGACATCGGAATCAGAACGATCAGCTGGACGAGAA	800
GAGGCTCTATCTGAACGGAAACCTGTCTTTGAAGGGCTTGGAAAGC	850
ACGAGGAATTCCCCGTTCTGGGGCAGGGCACCTTATCCATTGATGATA	900
AAAGACTTCAACCTCTGAAGTGGATCAACGCGAATTCTTCAGGACCTC	950
TCACTATCCTTACAGTGAAGAGTGGATCTGCCGACAGACTCGGAA	1000
TCCTTGTGATAGACGAAGCCCCGCACGTTGGTATCACAAGGTACCACTAC	1050
AATCCCCGAGACTCAGAAGATAGCAGAAGACAACTAAGAAGAACGATCGA	1100
CAGACACAAGAACCATCCCAGTGTGATCATGTGGAGTGTGGCGAACGAAAC	1150
CAGAGTCCAACCATCCAGACGCGGAGGGTTCTCAAAGCCTTATGAG	1200

FIGURE 4J

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ACTGCCAATGAAATGGATCGAACACGCCCGTGTATGGTGAGCATGAT 1250
GGACGCACCAGACGAGAGAACAGAGACGTGGCGCTGAAGTACTTCGACA 1300
TCGTCTGTGTGAACAGGTACTACGGCTGGTACATCTATCAGGGAAGGATA 1350
GAAGAAGGACTTCAAGCTCTGGAAAAGACATAGAAGAGCTATGCAAG 1400
GCACAGAAAGCCCACCTTTGTCACAGAATTGGTGCAGCGATAGCTG 1450
GCATCCACTACGATCCACCTCAAATGTTCTCCGAAGAGTACCAAGCAGAG 1500
CTCGTTGAAAAGACGATCAGGCTCCTTTGAAAAAAAGACTACATCATCGG 1550
AACACACGTGTGGGCCTTGAGATTTAAGACTCCTCAGAATGTGAGAA 1600
GACCCATTCTCAACCACAAGGGTGTTCACAAGAGACAGACAACCCAAA 1650
CTCGTTGCTCATGTACTGAGAAGACTGTGGAGTGAGGTT 1689

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BGUS	-----MLYPINTETRGVFDLNGVWNFKLDYG----KGLEEKWYESKLTDT---ISMAVP 47
HGUS	LGLOGGMLYPOESPSPRECKELDGLWSFRADFSNDNRRRGEEQWYRPLWESGPVDMPVP 60
EGUS	-----MLRPVETPTREIKKLDGLWAFSLDREN---CGIDQRWWESALQESR---AIAVP 48
 BGUS	 SSYNDIGVTKEIRNHIGYWYEREFTVPAYLKD---QRIVLRFSGSATHKAIVYVNGELVV 104
HGUS	SSFNDISQDWRLRHFVGWVYEREVILPERWTQDLRTVVLRIGSAHSYAIWVNGVDTL 120
EGUS	GSFNDQFADADIRNYAGNVWYQREVFIPKGWAG---QRIVLRFDAVTHYGKVWVNNQEVM 105
 BGUS	 EHKGGLPFEAEINNSLRDG---MNRVTAVDNILDDSTLPVG-LYSERHEEGLGVIR 159
HGUS	EHEGGYLPLFEADISNLVQVGPLPSRLRITIAINNTLPTTLPPGTIQYLTDTSKYPKGYF 180
EGUS	EHQGGYTPFEADVTPYVIAG---KSVRITVCVNNELNWQTIPPG--MVITDENGKKK--- 157
 BGUS	 -NKPNFDFFNYAGLHRPVKIYTTPTFYVEDISVVTDFNGPT--GTVTYTVDFQG-KAETV 215
HGUS	VQNTYFDFFNYAGLQRSVLLYTTPTTYIDDITVTTSVEQDS--GLVNYQISVKGSNLFKL 238
EGUS	-QSFHDFFNYAGIHRSVMLYTTPTNTWVDDITVVTHVAQDCNHASVDWQVVANG---DV 212
 BGUS	 KVSVVDEEGKVVASTEGLSGNVEIPNVILWEP----LNTYLYQIKVELVNDGLT---ID 267
HGUS	EVRLLDAENKVVVANGTGQQLKVPGVSLWWPYLMHERPAYLYSLEVQLTAQTS LGPVSD 298
EGUS	SVELRDADQQVATGQGTSGTLQVNPHLWQP----GEGYLYELCVTAKSQTEC---D 263
 BGUS	 VYEEPFGVRTVEVNDGFLINNKPFYFKGFGKHEDTPINGRGFNEASNVMDFNILKWIGA 327
HGUS	FYLPVGIRTVAUTKSQFLINGKPFYFHGVNKHEDADIRGKGFDWPLLVKDFNLLRWLGA 358
EGUS	IYPLRVRGIRSVAVKGEQFLINHKPFYFTGFRHEDALRGKGFDNVLMVHDHALMDWIGA 323
 BGUS	 NSFRTAHYPYSEELMRЛАДРЕГЛВИДЕТПАVGVHLNFМATTGLGEGSERVSTWEKIR-- 385
HGUS	NAFRTSHPYAAEVQMCDRYGIWVIDECPGVGLAL-----P-----QFFNNV 401
EGUS	NSYRTSHPYAAEMLDWADEHGIWVIDETAAVGFNLSLGIGFEAGNPKELYSEEAVNGE 383
 BGUS	 TFEHHQDVRELVS RDKNHPSVVMWSIANEAATEEEGAYEYFKPLVELTKELDPQKRPVT 445
HGUS	SLHHHMQVMEEVVRRDKNHPAVVMWSVANEPA SHLESAGYYLK MVIAHTKSLDPS-RPVT 460
EGUS	TQQ AHLQAIKELIARDKNHPSVVMWSIANEPDTRPQGAREYFAPLAEARTRKLDPT-RPIT 442
 BGUS	 IVLFVMMATPETDKVAELIDVIALNRYNGWYFDGGDLEAAKVHLRQEFHAWNKRCPGKPM 505
HGUS	FVS--NSNYAADKGAPYVDVICLNSYYSWYHDYGHLELIQLQLATQFENWYKKYQ-KPII 517
EGUS	CVNVMFCDAHTDTISDLFDVLCLNRYYGWYVQSGDLETAEKVLEKELLAWQEKLH-QPII 501
 BGUS	 ITEYGA DT VAG FHD ID PVM FTE EY QV E YY QAN HVV FD -- EFENFVG EQ AWN FADFAT SQG 563
HGUS	QSE YGA ET IAG FHD PPL MFT EY QK SLL E QY HL GLD QK RR KYY V GEL I WNFADF MTEQS 577
EGUS	ITEYGVDTLAGLHS MY TDMW SEE YQC AWL DMY HR VFD -- RVS AVV GEQ VWN FADFAT SQG 559
 BGUS	 VMRVQGNKKGVTRDRKPKLAAHVFRERWTNIPDFGYKN----- 602
HGUS	PTRVLGNKKGIFT RQR QPKSAAFLRERYWKIAN-ET----- 613
EGUS	ILRVGGNKKGIFT RDRKPKSAAFLLQKRWTGMNFGEKPQQGGKQ 603

FIGURE 5.

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Staphylococcus	MVDLTSILYPINTETRGVPDENGVWNFKLDYK-KGLEEKWYESKLTDTISMAVPSST	: 55
Staph_homi	-	-
Staph_warm	--LXLLHPIITGTRGGFALYGXXNLMDYK-XGLTDWTXTSLLTLSRLVVLWSWT	: 52
Thermotoga	--MVRPORNICKREFILILNGVWNLEVTSK-----D-RPAVPGSW	: 36
Enb/Salmon	--	-
E_coli	--MGRPVETPTREIKGLDGLWAFSLDRENCGIDQRWWESALQESRAIAVPGSF	: 51
Staphylococcus	NDIGVTKEIRNHIGYVWYEREFTVPAVLKDQR--IVLRFGSATHKAIYVNGELVV	: 109
Staph_homi	-	-
Staph_warm	THX-LTGEK-PAISIILWPNSELTVSXLYXGSLXSSXLCSLTXHVVICQXVTLKV	: 106
Thermotoga	NEQ-YQDLCYEEGPFTYKTTFYVPKXLSQKH--IRLYFAAVNTDCEVFLNGEKVG	: 88
Enb/Salmon	--	-
E_coli	NDQFADADIRNYAGNVWYQREVFIPKGWAGQR--IVLRFDAVTHYKGKVVNNQEVH	: 105
Staphylococcus	EHKGGFLPPEAEIN-NSLRDGMRVTVAVDNIEDDOSTLPVGLYSRHEEGLGKVR	: 164
Staph_homi	-	-
Staph_warm	DHTGLIJKFEPMSTTCXXDELVTGTAX--IEYHXLPHGLYRCKMEKXGLGKCNF	: 160
Thermotoga	ENHIEYLPFEVDVIGKVKSGENELRVVVEN-RLKVGGEPSKVPDSTHTVGFEGSF	: 143
Enb/Salmon	--	-
E_coli	EHQGGYTPHEADVTPYVIAGKSVRITVCVNNELNWQTIPPGMVITDENG---KCK	: 157
Staphylococcus	NKPNFDEPNYAGIHRPVKEYTPTVYEVNSVDFNGP---TGTVTYTVDFOQKA	: 217
Staph_homi	-	-
Staph_warm	YXLHFAFEKYAKXILRTVXMYX-NLVRXQH--JYDX-HK---HK-TVEQCQDN-	: 206
Thermotoga	PPANFDFEPYGGIIRPV,LEFTOHARILQHSESEPEIKLGKVKVKEVSEEA	: 199
Enb/Salmon	--GKLSPTPTAYCQHDXK-DVLEN--TEQATVLGKVGADG	: 37
E_coli	QSYFHDEPNYAGIHRSVMEYTPNTWVQDITVQHVAQD--CNHASVWDQVYVANG	: 210
Staphylococcus	ET--VXISVMEEGKVVASTELSNSVTEPVVNRVLTPLNTLQHTELVNDGLTI	: 271
Staph_homi	--	-
Staph_warm	--SLSNSVTEPVVNRVLTPLNTLQHTELVNDGLTI	: 35
Thermotoga	KIKSVQHILPENDHAKESESACQNVITQPHIPLQPHAHVNM-VELLNINNECV	: 262
Enb/Salmon	VGQEMTJHOGCEKEKCIKTSNRVEREPIIEMAREPSLEDPPLPPTVLELEKD---	: 251
E_coli	D---IPVDPDQOCGLVAQGLATIIFEDMPH-EPGEGYIEMVTCAN-GEC	: 89
	D---MSLPIRSDQQVWATGQTSITLQVMPHOPGEGHIELECTAXSQ-TEC	: 262
Staphylococcus	EVIEEPFVWVTEVNDGKDIINNIEAIIKCFKHEITPINFVNEASNM-FML	: 327
Staph_homi	EVIEEPFVWVTEVNDGKATIINNIEAIIKCFKHEITPINFVNEASNM-FML	: 91
Staph_warm	EVIEEPFVWVTEVNDGKATIINNIEAIIKCFKHEITPINFVNEASNM-FML	: 317
Thermotoga	-ETLIDHIRTISWDEKALIINGKIVLKEFQHETPINFVPLMKTIFML	: 306
Enb/Salmon	DEPVRVHIIKSIITXXKGEQMLIINHKEPLTSHGRHEIADFRIHADPVLMLHHAHM	: 145
E_coli	QIPPLRVEIREAVKGEQPHIMHKEPLTSHGRHEIADFRIHADPVLMLHHAHM	: 318
Staphylococcus	AEIGAIEFFHAAHYI-SSEELMLRILREGILVVDLSTPAVWH-BNFMMATTGLGEGSER	: 382
Staph_homi	AEIGAIEFFHAAHYI-SSEELMLRILREGILVVDLSTPAVWH-BNFMMATTGLGEGSER	: 146
Staph_warm	KVGAIEFFHAAHYI-SSEELMLRILREGILVVDLSTPAVWH-BNFMMATTGLGEGSER	: 369
Thermotoga	KVNAIEFFTSIHYI-SSEELMLRILREGILVVDLSTPAVWH-BNFMMXTLGGSX---A	: 348
Enb/Salmon	KVNAIEFFTSIHYI-SSEELMLRILREGILVVDLSTPAVWH-BNFMMXTLGGSX---A	: 201
E_coli	DEIGAIEFFHAAHYI-SSEELMLRILREGILVVDLSTPAVWH-BNFMMXTLGGSX---A	: 373
Staphylococcus	HSAVWIKERTFE--HMQDVLREKVSIDKHNIPSVVNPSSAIIAEEEGYVHNGD	: 435
Staph_homi	HSAVWIKERTFE--HMQDVLREKVSIDKHNIPSVVNPSSAIIAEEEGYVHNGD	: 199
Staph_warm	HSAVWIKERTFE--HMQDVLREKVSIDKHNIPSVVNPSSAIIAEEEGYVHNGD	: 422
Thermotoga	HQHKEFDOTLE--FKEKEVDCGIXFKEKIAWVTFQGXHGXNKGEKAKGEDE	: 398
Enb/Salmon	HYNPKTOKIA--DNRTRDIDFKEVDCGIXFKEKIAWVTFQGXHGXNKGEKAKGEDE	: 257
E_coli	EVYSDAINGETSQAQIQLAQIYIAPKTHPSVCCSITMFDPDRPNCGRVYABJ	: 428
	EVYSDAINGET-QQAEIQLAQIYIAPKTHPSVCCSITMFDPDRPNCGRVYABJ	
Staphylococcus	VELTKELIPOKGETVILFVMAT--PETEKVAEIIETVIALEKINLTFDQELEAK	: 489
Staph_homi	GGAAJELIPOKGETVILFVMAT--PETEKVAEIIETVIALEKINLTFDQELEAK	: 253
Staph_warm	VNLAGISKDCOOCKVLIITILYCAK--RNVCCEXGIVVQDQOQXQSPLEGE	: 476
Thermotoga	YETANEMIR-TEPVVM-SMMMDAERTDTRALKVYHUTIYQHTRHEG	: 453
Enb/Salmon	AKATRBLIP-TSPITCVMVFCD-AESDTTTSIFUVVCHMRVYHUTVQS-ELHKA	: 310
E_coli	AEATRBLIP-TSPITCVMVFCD-AHBTBTISQIFUVVCHMRVYHUTVQS-ELHKA	: 481
Staphylococcus	KVHIIROEFHAFHGNKCPGKIDGITEVACTPF-FHDIDEVVPHEDVQVZVYQANHVI	: 545
Staph_homi	KVHIIROEFHAFHGNKCPGKIDGITEVACTPF-FHDIDEVVPHEDVQVZVYQANHVI	: 309
Staph_warm	IKAQDQKEVWQXQXN-IMKMEIETVWVXKV-LQOXPDMKXPPE-KMXYKGYXK	: 532
Thermotoga	LQAIEKIEELYAHR-IMKMEIETVWVXKV-LQOXPDMKXPPE-KMXYKGYXK	: 508
Enb/Salmon	EQMIEQHLLAQOSLHL-IMKMEIETVWVXKV-LQOXPDMKXPPE-KMXYKGYXK	: 365
E_coli	EVKUDEKLLLAQOSLHL-OEIIETVWVXKV-LQOXPDMKXPPE-KMXYKGYXK	: 536
Staphylococcus	FGEFENFVGEOAWNFAADFATSGQVMRVQGNIGGVFTRDRKPKLAAHVFRERWTNIP	: 601
Staph_homi	FGEFENFVGEOAWNFAADFATSGQVMRVQGNIGGVFTRDRKPKLAAHVFRERWTNIP	: 365
Staph_warm	FGEFENFVGEOAWNFAADFATSGQVMRVQGNIGGVFTRDRKPKLAAHVFRERWTNIP	: 535
Thermotoga	LLKEDYIIGTHWVAFADEKTPQNYVRPILNHKGVFTDRDROPXLVAVLRLW9EV-	: 563
Enb/Salmon	FPRG SVC--	: 372
E_coli	FPRVSAVVGEOAWNFAADFATSGQILRVGGNORGIFTDRKPKSAFLQKRWTGMN	: 592
Staphylococcus	DFGYKN----- : 607	
Staph_homi	DFGYKNASHHH : 376	
Staph_warm	----- : -	
Thermotoga	----- : -	
Enb/Salmon	----- : -	
E_coli	FGEKPQGGKQ : 603	

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Secretion of GUS^{Stp} in *E. coli*

Cellular fractions were assayed for glucuronidase and galactosidase activity

Secretion Index was calculated as follows:

- percent of total activity in the periplasm fraction for glucuronidase and galactosidase was calculated

- galactosidase value was subtracted from glucuronidase as "contamination"

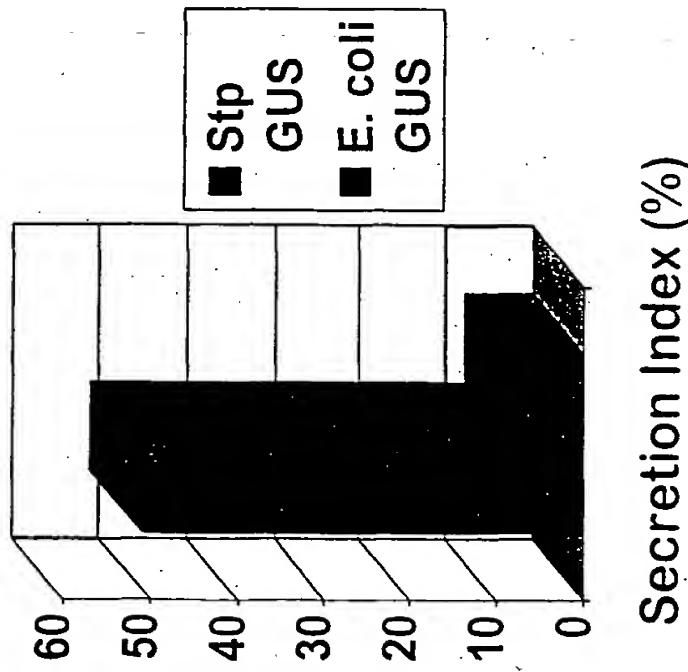


FIG. 6

Thermal stability of β -glucuronidases

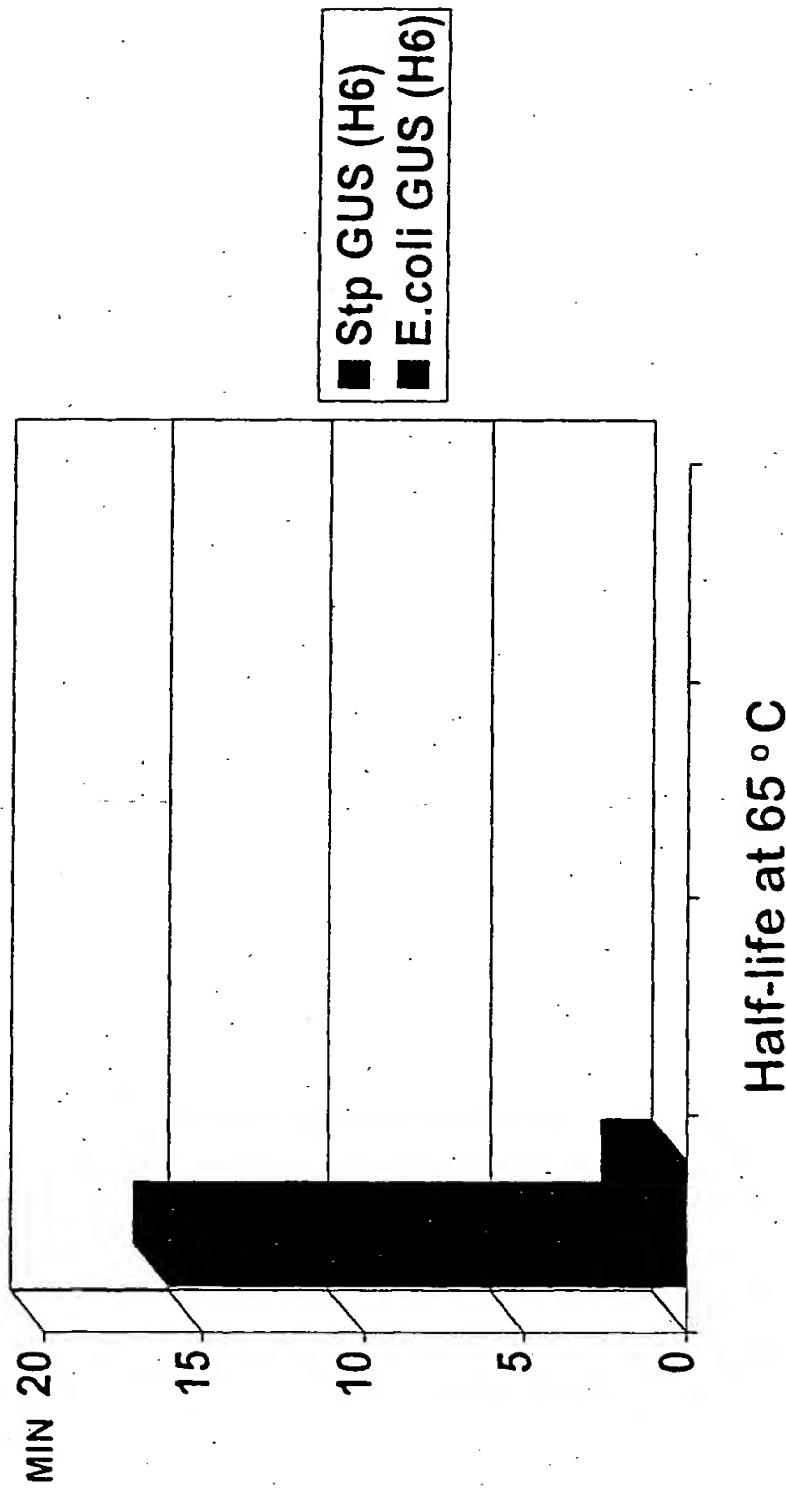


FIG. 7

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Turnover number (37°C)

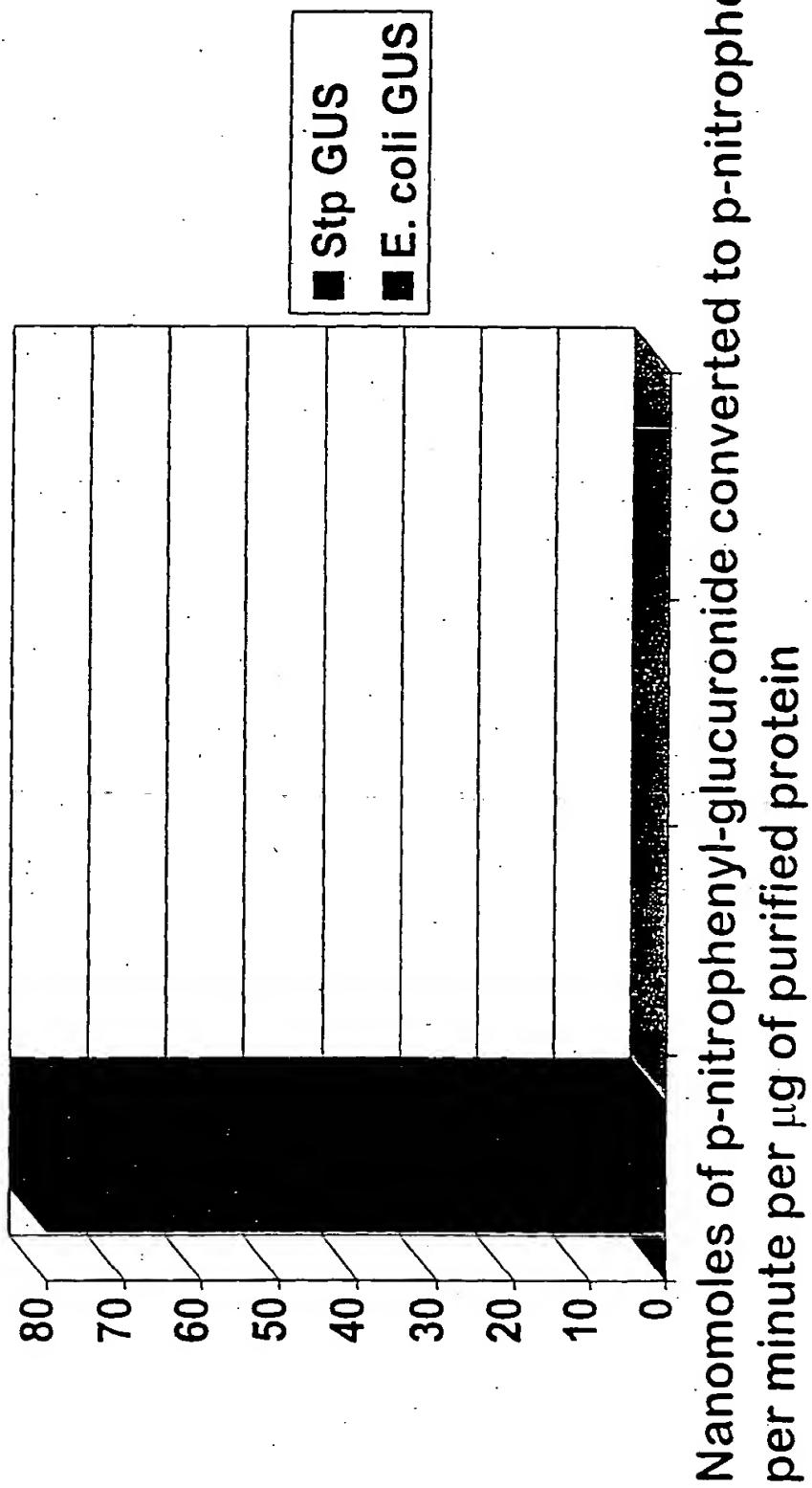
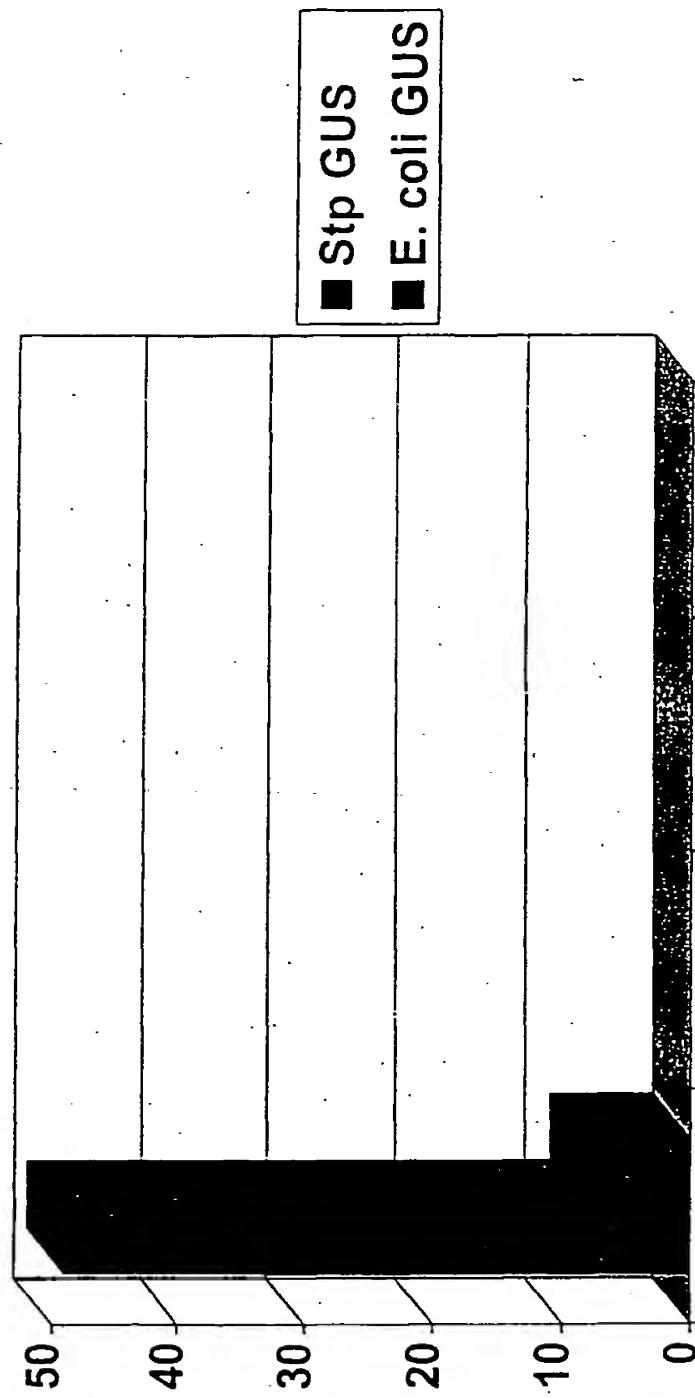


FIG. 8

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Turnover number (RT)



Nanomoles of p-nitrophenyl-glucuronide converted to p-nitrophenyl
per minute per μ g of purified protein

FIG. 9

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Effect of detergents on $\text{GU}\text{S}^{\text{stop}}$ activity

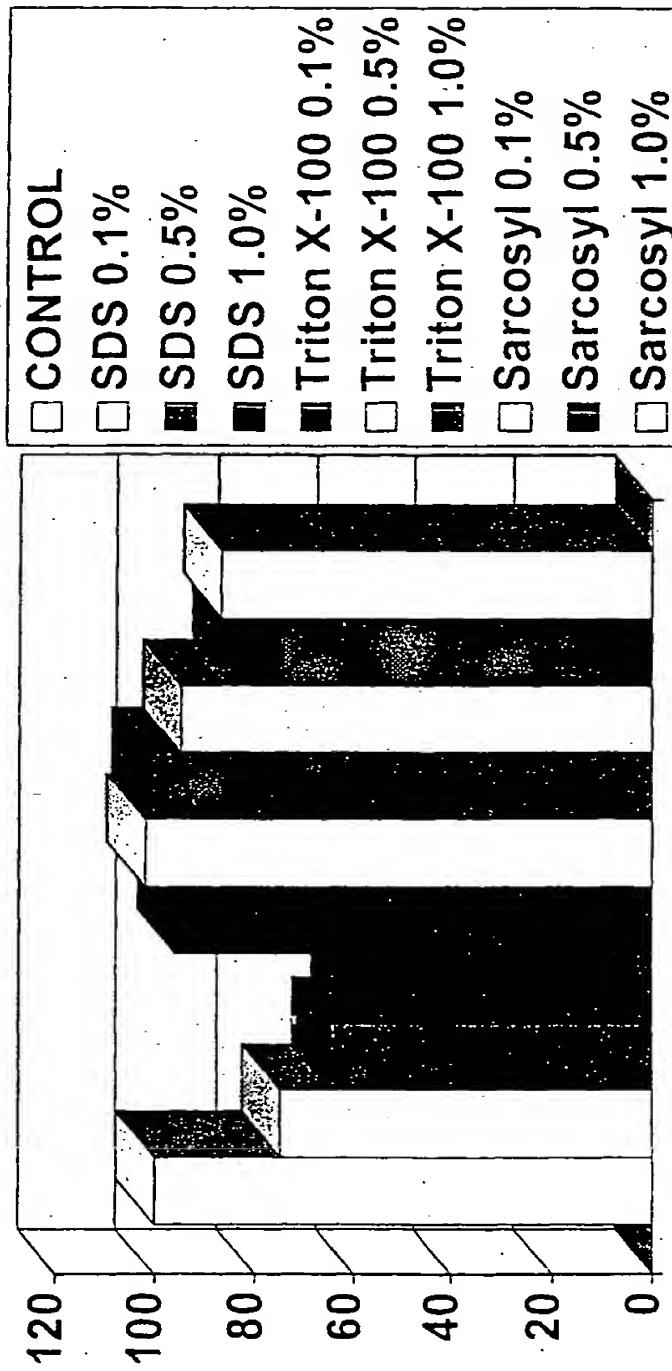
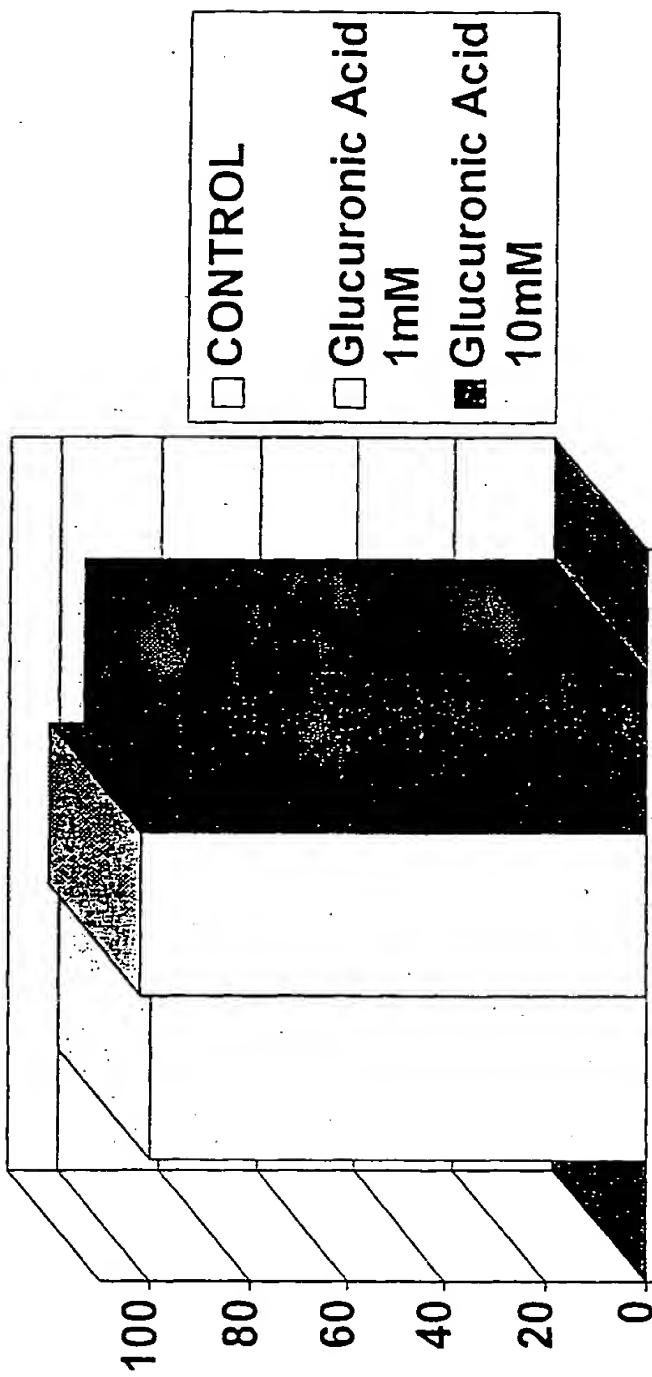


FIG. 10

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Effect of glucuronic acid, the reaction product, on GUS^{sup} activity



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GUS_{stop} activity in salt and in different organic solvents

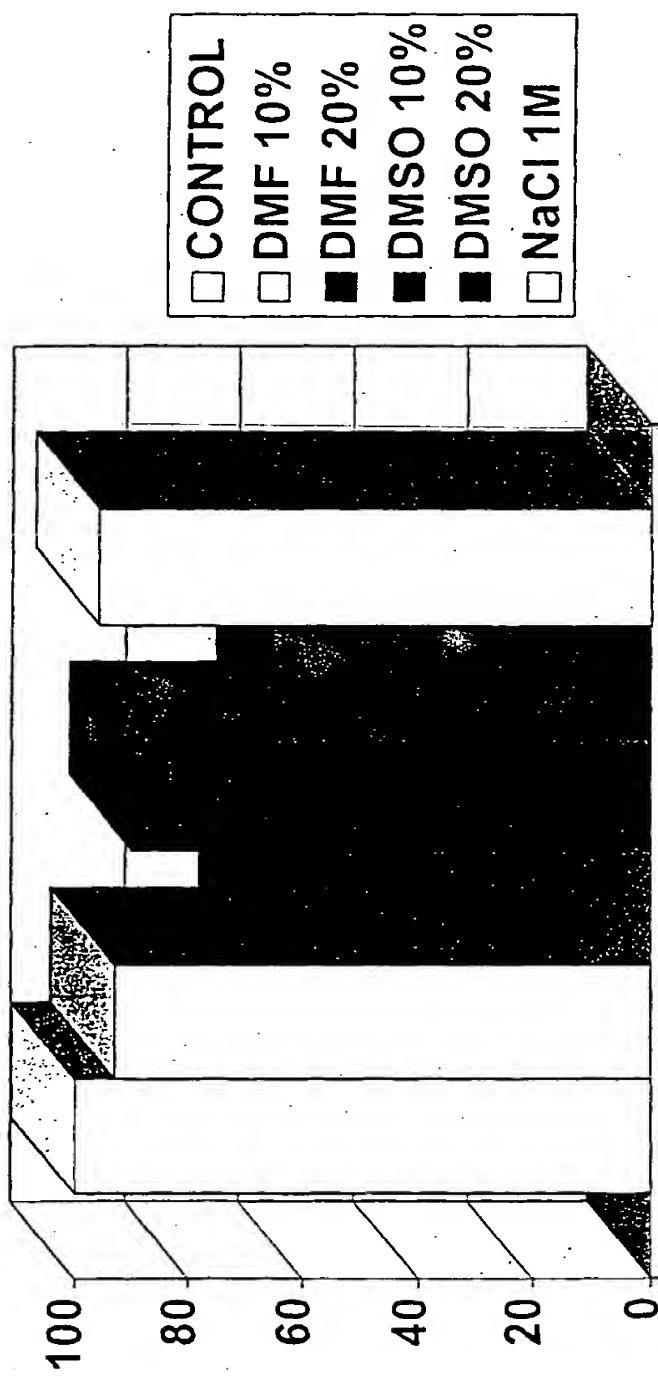


FIG. 12

FIGURE 13A

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MetValAspLeuThrSerLeuTyr
 ATACGACTCA CTAGTGGGTC GACCCATGGTAGATCTGACTAGTCTGTAC
 SalI NcoI BglII

ProIleAsnThrGluThrArgGlyValPheAspLeuAsnGlyValTrpAsn
 CCGATCAACACCGAGACCGTGGCGTCTCGACCTCAATGGCGTCTGGAAC

PheLysLeuAspTyrGlyLysGlyLeuGluGluLysTrpTyrGluSerLys
 TTCAAGCTGGACTACGGAAAGGACTGGAAGAGAAGTGGTACGAAAGCAA

LeuThrAspThrIleSerMetAlaValProSerSerTyrAsnAspIle
 GCTGACCGACACTATTAGTATGGCCGTCCAAGCAGTTACAATGACATTG

GlyValThrLysGluIleArgAsnHisIleGlyTyrValTrpTyrGluArg
 GCGTGACCAAGGAAATCCGCAACCATAATCGGATATGTCCTGGTACGAACGT

GluPheThrValProAlaTyrLeuLysAspGlnArgIleValLeuArgPhe
 GAGTTCACGG TGCCGGCCTATCTGAAGGATCAGCGTATCGTGCCTCGCTT

GlySerAlaThrHisLysAlaIleValTyrValAsnGlyGluLeuVal
 CGGCTCTGCAACTCACAAAGCAATTGTCTATGTCAATGGTGAGCTGGTCG

ValGluHisLysGlyGlyPheLeuProPheGluAlaGluIleAsnAsnSer
 TGGAGCACAGGGCGGATTCCCTGCCATTGCAAGCGGAAATCAACAACCTG

LeuArgAspGlyMetAsnArgValThrValAlaValAspAsnIleLeuAsp
 CTGCGTGATGGCATGAATCGCGTCACCGTCGCCGTGGACAACATCCTCGA

AspSerThrLeuProValGlyLeuTyrSerGluArgHisGluGluGly
 CGATAGCACCCCTCCCGGTGGGCTGTACAGCGAGCGCCACGAAGAGGGCC

LeuGlyLysValIleArgAsnLysProAsnPheAspPhePheAsnTyrAla
 TCGGAAAAGTCATTGTAACAGCCGACTTCGACTTCTCAACTATGCA

GlyLeuHisArgProValLysIleTyrThrThrProPheThrTyrValGlu
 GGCCTGCACCGTCCGGTAAAACTACACGACCCGTTACGTACGTGCGA

AspIleSerValValThrAspPheAsnGlyProThrGlyThrValThr
 GGACATCTCGGTTGTGACCGACTTCATGGCCAACCGGGACTGTGACCT

TyrThrValAspPheGlnGlyLysAlaGluThrValLysValSerValVal
 ATACGGTGGACTTCAGGCAAAGCCGAGACCGTGAAAGTGTGGTCTGGT

AspGluGluGlyLysValValAlaSerThrGluGlyLeuSerGlyAsnVal
 GATGAGGAAGGCAAAGTGGTCGCAAGCACCGAGGGCCTGAGCGGTAAACGT

GluIleProAsnValIleLeuTrpGluProLeuAsnThrTyrLeuTyr
 GGAGATTCCGAATGTCATCCTCTGGGAACCACTGAAACACGTATCTCTACC

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FIGURE 13B

GlnIleLysValGluLeuValAsnAspGlyLeuThrIleAspValTyrGlu
 CAGATCAAAGTGGAACTGGTGAACGACGGACTGACCATCGATGTCTATGAA

GluProPheGlyValArgThrValGluValAsnAspGlyLysPheLeuIle
 GAGCCGTCGGCGTGC GGACCGTGGAA GTCAACGACGGCAAGTCCCTCAT

AsnAsnLysProPheTyrPheLysGlyPheGlyLysHisGluAspThr
 CAACAACAAACCGTTCTACTTCAAGGGCTTGCAAAACATGAGGACACTC

ProIleAsnGlyArgGlyPheAsnGluAlaSerAsnValMetAspPheAsn
 CTATCAACGGCCGTGGCTTAACGAAGCGAGCAATGTGATGGATTTCAT

IleLeuLysTrpIleGlyAlaAsnSerPheArgThrAlaHisTyrProTyr
 ATCCTCAAATGGATCGCGCCAACAGCTCCGGACCGCACACTATCCGTA

SerGluGluLeuMetArgLeuAlaAspArgGluGlyLeuValValIle
 CTCTGAAGAGTTGATGCGTCTGGCGATCGCGAGGGCTGGTCGTGATCG

AspGluThrProAlaValGlyValHisLeuAsnPheMetAlaThrThrGly
 ACGAGACTCCGGCAGTTGGCGTGCACCTCAACTTCATGGCCACCACGGGA

LeuGlyGluGlySerGluArgValSerThrTrpGluLysIleArgThrPhe
 CTCGGCGAAGGCAGCGAGCGCTCAGTACCTGGAGAAGATTGGACGTT

GluHisHisGlnAspValLeuArgGluLeuValSerArgAspLysAsn
 TGAGCACCATCAAGACGTTCCGTGAACTGGTGTCTCGTGACAAGAAC

HisProSerValValMetTrpSerIleAlaAsnGluAlaAlaThrGluGlu
 ATCCAAGCGTCGTGATGTGGAGCATTGCCAACGAGGCAGCGACTGAGGAA

GluGlyAlaTyrGluTyrPheLysProLeuValGluLeuThrLysGluLeu
 GAGGGCGCGTACGAGTACTTCAAGCCGTTGGAGCTGACCAAGGAAC

AspProGlnLysArgProValThrIleValLeuPheValMetAlaThr
 CGACCCACAGAACGGCTCCGGTACGATCGTGTGTTGTGATGGCTACCC

ProGluThrAspLysValAlaGluLeuIleAspValIleAlaLeuAsnArg
 CGGAGACGGACAAAGTCGCCGAACTGATTGACGTACCGCCTCAATCGC

TyrAsnGlyTrpTyrPheAspGlyGlyAspLeuGluAlaAlaLysValHis
 TATAACGGATGGTACTTCGATGGCGGTGATCTCGAACGCGGCCAAAGTCCA

LeuArgGlnGluPheHisAlaTrpAsnLysArgCysProGlyLysPro
 TCTCCGCCAGGAATTTCACGCGTGGAACAGCGTTGCCAGGAAAGCCGA

IleMetIleThrGluTyrGlyAlaAspThrValAlaGlyPheHisAspIle
 TCATGATCACTGAGTACGGCGCAGACACCGTTGCGGGCTTCACGACATT

AspProValMetPheThrGluGluTyrGlnValGluTyrTyrGlnAlaAsn
 GATCCAGTGATGTTCACCGAGGAATATCAAGTCGAGTACTACCAGGCGAA

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FIGURE 13C

HisValValPheAspGluPheGluAsnPheValGlyGluGlnAlaTrp
CCACGTCGTGTTGATGAGTTGAGAACTTCGTGGGTGAGCAAGCGTGGA

AsnPheAlaAspPheAlaThrSerGlnGlyValMetArgValGlnGlyAsn
ACTTCGCGGACTTCGCGACCTCTCAGGGCGTATGCGCGTCCAAGGAAAC

LysLysGlyValPheThrArgAspArgLysProLysLeuAlaAlaHisVal
AAGAAAGGGCGTGTTCACTCGTGACCGCAAGCCGAAGCTCGCCGCGCACGT

PheArgGluArgTrpThrAsnIleProAspPheGlyTyrLysAsn
CTTTCGCGAGCGCTGGACCAACATTCCAGATTCCGGCTACAAGAACGCTA

SerHisHisHisHisHisVal *
GCCATCACCATCACCATCACGTGTGAATTGGTGACCG
NheI PmlI BstEII

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FIGURE 14

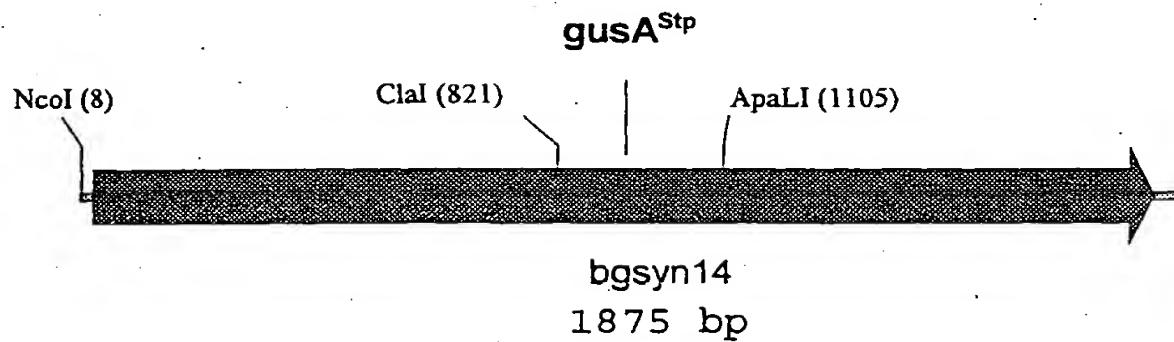
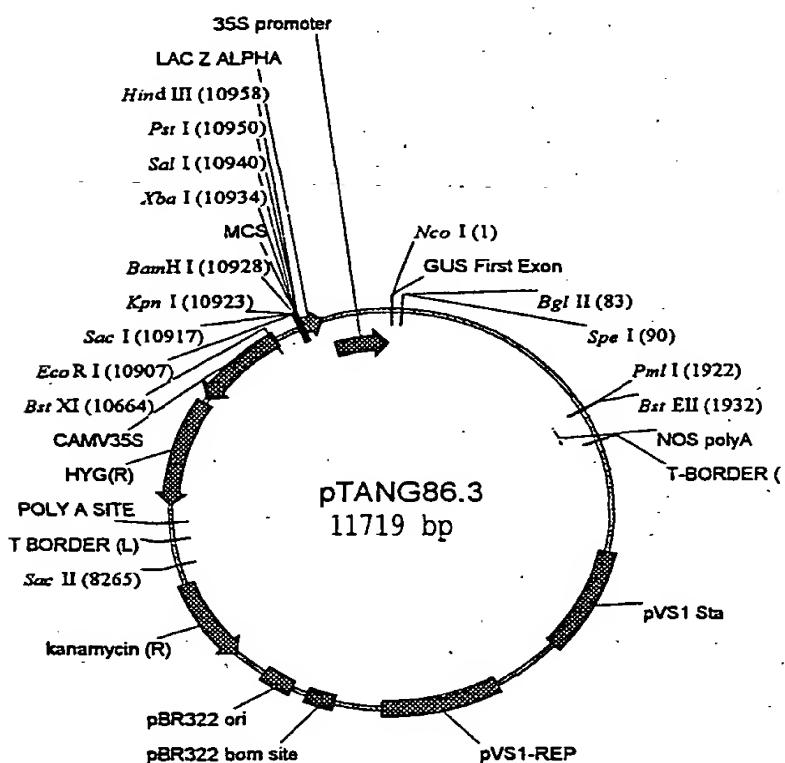
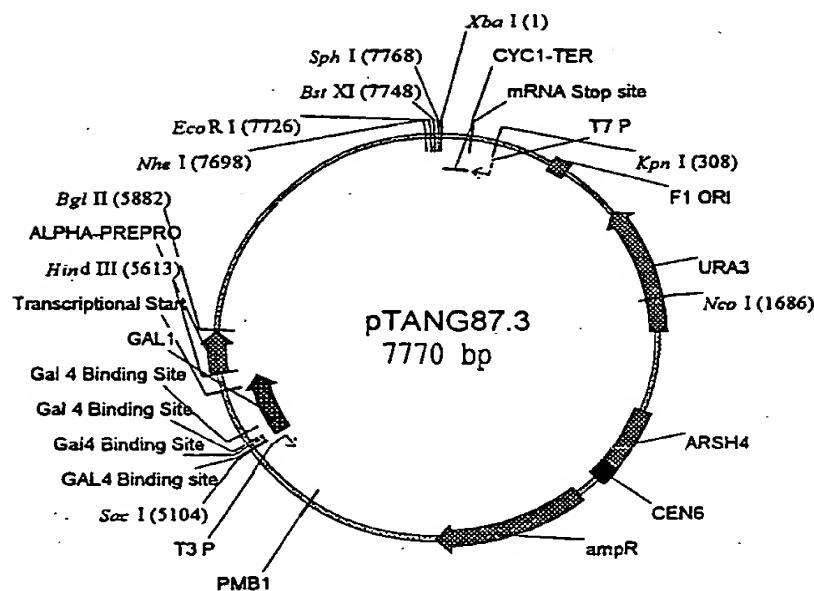


FIGURE 15

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FIGURE 16

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1 ATGTTACGTT CTGTCGAAAC CGCGACGCAGA GAAATCAAAA AACTGGACGG
51 CCTGTGGTCG TTTTGTATGG ATAGCGAAGA GTGCGGCAAC GCGCAGCAAT
101 GGTGGCGTCA ACCGTTACCC CAAAGCCGCG CTATGCCGT TCCGGGAAGC
151 TATAACGATC AGTTTGCCGC TGCCGAGATC CGCAATTATG TTGGCAACGT
201 CTGGTATCAG CGTGAGATAC GCATCCCGAA AGGCTGGGAT CGCCAGCGCA
251 TAGTGCTGCG CTTTGATGCG GTGACTCACT ATGGAAAAGT TTGGGTCAAT
301 GACCAATTAA TAATGGAACA TCAGGGCGGC TACACGCCGT TTGAAGCGGA
351 TATCAGCCAC CTTATCTCCC CCGGGGAATC CGTGGCTATC ACGGTATGCG
401 TGAATAACGA GCTGAACTGG CAGACGATCC CGCCGGCGT TGTGACCCAG
451 GGCCTAAACG GTAAGAAGCA GCAAGCGTAT TTCCATGATT TCTTTAACTA
501 CGCCGGTATT CATCGCAGCG TAATGCTGTA CACCACGCCG AAAACTTTG
551 TGGAAGATAT TACCGTCGTG ACGCAGGTG CTGACGATCT GGCTCAGGCT
601 ACCGTCGCCT GGCAGGTACG GGCAGAATGGC GAAGTGGCTG TAGAGCTACG
651 TGACGCGGAG CAACAGCTTG TCGCTTCGGG GCAAGGGGAA AAAGGTGAAC
701 TGCTGCTGGA AGGGCCGCGG CTGTGGCAGC CTGGCGAGGG CTATCTTAT
751 GAACTGCGGG TCATCGCGCA GCATCAGGAC GAGCAGGATG AATATCCGCT
801 GCGCGTCGGT ATTGCGTCGG TAGAAGTAAA AGGGGAGGAG TTCCTGATCA
851 ACCATAAGCC TTTCTATTTTC ACCGGGTTCG GACGTCACTGA AGATGCCGAT
901 CTGCGGGTA AGGGTTTTGA TAACGTGCTG ATGGTGCACG ACCACGCGCT
951 AATGGACTGG ATCGGTGCGA ACTCTTACCG TACCTCGCAT TACCCCTTATG
1001 CCGAAGAGAT GCTCGACTGG GCGGACGAAC ATGGCATCGT CATCATTGAT
1051 GAAACGGCCG CCGTCGGATT CAACCTGTCT TTAGGGATTA GCTTTGATGT
1101 CGGCGAAAAA CCCAAAGAGC TCTACAGCGA TGAGGCCGTG AACGATGAAA
1151 CGCAGCGCGC GCACCTGCAAG GCAATTAAAGG AGCTGATTGC CCGCGATAAG
1201 AACCAACCAA GCGTCGTGAT GTGGAGTATC GCCAACGAAC CGGATAACCG
1251 CCCGAACGGC GCGCGCGAAT ACTTCGCTCC GCTGGCGCAG GCAACGCGCG
1301 AACTCGATCC TACACGTCCG ATAACCTGCG TGAACGTGAT GTTCTGCGAT
1351 GCGGAAAGCG ACACCAATTAC CGATCTCTT GATGTCGTTT GCCTGAACCG
1401 CTACTACGGC TGGTATGTAC AAAGCGGCGA TCTGGAGAAG GCTGAGAAAG
1451 TGCTGGAGAA AGAGCTTCTG GCCTGGCAGG AGAAAATCCA CCGCCCCGATT
1501 ATCATCACCG AATACGGCGT CGATAACGCTT GCAGGCCCTGC ATTCCATGTA
1551 CAACGATATG TGGAGCGAAG AGTACCACTG CGCCTGGCTT GATATGTACC
1601 ATCGCGTGTG TGATCGCGTC AGCGCCGTCG TCGGCGAGCA GGTATGGAAC
1651 TTGCGCGACT TCGCCACTTC GCAGGGCATT ATGCGCGTTG GCGGCAACAA
1701 AAAAGGTATA TTGACCCCGCG ACAGAAAACC AAAATCGGCG GCCTTCCCTGC
1751 TGCAAAAACG CTGGACCGGC ATGGACTTTG GCGTGAAGCC CCAGCAGGGGA
1801 GATAAATAAT GA

```

FIGURE 17

1 MLRSVETATR EIKKLDGLWS FCMDSEECGN AQQWWRQPLP QSRAIAVPGS
51 YNDQFAAAEI RNYVGNVWYQ REIRIPKGWD RQRIVLRFDA VTHYGKVWVN
101 DQFLMEHQGG YTPFEADISH LISAGESVRI TVCVNNELNW QTIPPGVVTO
151 GVNGKKQQAY FHDFFNYAGI HRSVMLYTTP KTFVEDITVV TQVADDLAQA
201 TVAWQVRANG EVRVELRDAE QQLVASGQGE KGELLLEGPR LWQPGEGYLY
251 ELRVIAQHQA EQDEYPLRVG IRSVEVKGEQ FLINHKPFYF TGFRHEDAD
301 LRGKGFDNVL MVHDHALMDW IGANSYRTSH YPYAEEMLDW ADEHGIVIID
351 ETAAVGFNLS LGISFDVGEK PKELYSDEAV NDETQRAHLQ AIKELIARDK
401 NHPSVVMWSI ANEPDTRPNG AREYFAPLAQ ATRELDPTRP ITCVNVMFCD
451 AESDTITDLF DVVCLNRYYG WYVQSGDLEK AEKVLEKELL AWQEKLHRPI
501 IIITEYGVDTL AGLHSMYNDM WSEYYQCAWL DMYHRVFDRV SAVVGEQVWN
551 FADFATSQGI MRVGGNKKGI FTRDRPKSA AFLLQKRWTG MDFGVKPQQG
601 DK

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Staph	: MVDLTSLYPINTETRGVFDLNQVNFKIDYD-G-KLE	: 35
E coli	: -----MLRPVETPTREIKKLDGIWASSIDRENCGID	: 31
Sal	: -----MLRSVETATREIKKLDGIWSPCMDSEECGNA	: 31
Staph	: EKWWYESKLTDТИСМАВFSSYNDIGVTKEIRNHICV	: 71
E coli	: QRWMEСALQESRAJAVЕGСFNDQFADADIRNYAGMV	: 67
Sal	: QQWWRQPLPQSRATAVЕGСSYNDQFAAAEIRNYVGIV	: 67
Staph	: WYEREFTVЕAYLKDQRIVLRFGSATHKAIIVYVNGEL	: 107
E coli	: WYCREVFIPKGWAGQRIVLRFDAVTHYGVVVVNNOE	: 103
Sal	: WYCREIRHPKGWDRQRIVLRFDAVTHYGVVVVNDQF	: 103
Staph	: VMEHGGFLPFEAEINNSLRDGМN-RVTVAVDNILD	: 142
E coli	: VMEHGGYTPFEADVTPYVIAGKSVRITVCVNNELN	: 139
Sal	: LMEHGGYTPFEADISHLISAGESVRITVCVNNELN	: 139
Staph	: DSTLPVGLYSERHEEGLGKVIRNKPNTDFNYAGLH	: 178
E coli	: WOTIPEPGMVITDEN---GKKQS-YFHDFPNYAGIH	: 171
Sal	: WOTIPEPGVWTQGVN---GKKQQA-YFHDFPNYAGIH	: 171
Staph	: RPKIYTTFETIYVEDISVVTDFNGPTGTVFYTVDFQ	: 214
E coli	: RSVMLYTTENIWWDDITIVVTHVAODCNHASVWDQWV	: 207
Sal	: RSVMLYTTETKTFVEDITIVVTQVADDLAQATVAWQVR	: 207
Staph	: GKAETVKVISVVDEEGKWAСTEGLSGNVEIPNVILW	: 250
E coli	: ANGD-VSVELRDADQQVVAATGQQGTSGTLQVNVPHLW	: 242
Sal	: ANGE-VRVELRDABQQLVASGQGEKGEELLLEGPRlw	: 242
Staph	: EPLNTYLYQIKVELVNDGLTIDVYEEPFGVRTVEWN	: 286
E coli	: QPGEGYLYELCVTAKSQ-TECDIYPLRVGERSVAWK	: 277
Sal	: QPGEGYLYELRVIAQHQ-DEQDEYPLRVGIRSVEWK	: 277

FIG. 18A

Staph : DGKFLINNKPFYFKGFGKHEDTPINGRGNEASNVM : 09/936759
E coli : GEQFLINHKPFYFTGFGGRHEDADLRGKGFDNVLMVE : 313
Sal : GEQFLINHKPFYFTGFGGRHEDADLRGKGFDNVLMVE : 313

Staph : DFNILKWIGANSRTAHPYSEEMLRLADREGLVMI : 358
E coli : DHALMDWIGANSYRTSHYPYAEEMLDWADEHCIVMI : 349
Sal : DHALMDWIGANSYRTSHYPYAEEMLDWADEHCIVMI : 349

Staph : DETPAVGVLNFMMATTGLGEGSERVSTWEKIR--TF : 392
E coli : DETAAVGPNLISLGIGFEAGNPKELYSEAVNGETC : 385
Sal : DETAAVGPNLISLGISEDVGEKPKELYSDAEVNDETC : 385

Staph : EHHDQDVLRELVS RDKNHPSVVMWSIANEAATEEEGA : 428
E coli : QAHLOQAIKELIARDKNHPSVVMWSIANEPDTREOGA : 421
Sal : RAHLOQAIKELIARDKNHPSVVMWSIANEPDTREOGA : 421

Staph : YEYFKPLVELTKELDEOKRFVTIVLFVMATPETDKV : 464
E coli : REYFAPLAEAATRKLDPETRPITCVNMFCDAHEEDTI : 456
Sal : REYFAPLAQAATRELDP-TRPITCVNMFCDAESDTI : 456

Staph : AELIDVIALNRVNGWYFDGGDLEAAKVHERQEFHAW : 500
E coli : SLDLEDVLCLNRYYGWYVQSGDLETAEKVLEKELLAW : 492
Sal : TDLEDVWCLNRYYGWYVQSGDLEKAEKVLEKELLAW : 492

Staph : NKRCPGKPIMITEYGADEVAGFHIDIPVMFTEEYCV : 536
E coli : QEKHH-QPIIITEYGVDTLAGLHSMYTDMWSEYQC : 527
Sal : QEKHH-RPIIITEYGVDTLAGLHSMYNDMWSEYQC : 527

Staph : EYYQANHVVFDEFENEVGEGQAWNFAADFATSQGVMRV : 572
E coli : AWEDMYHRVFDRAVVGEOQVWNFADFATSQGILRV : 563
Sal : AWEDMYHRVFDRAVVGEOQVWNFADFATSQGIMRV : 563

FIG. 18B

Staph : QGNKKGVFERDRKPKLAAHVFRERHTNIPDFGYKN-
E coli : GGNKKGEFFTRDRKPKSAAFLLQKRWTGM-NFGERKPC : 598
Sal : GGNKKGEFFTRDRKPKSAAFLLQKRWTGM-DFGVKPO : 598

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Staph : ----- : -
E coli : QGGKQ-- : 603
Sal : QGDK--- : 602

FIG. 18C

Staph	:	-----	ATGCTAGATCTGACTAGTCCTGTACCC	
E.coli	:	TTATTATCTTAA	TGAGGAGTCCTTATGTTACGTCC	
Sal	:	-----	ATGETACGTTC	

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Staph	:	GATCAACACCGAGACCCGTGGCTCTTCCACCTCAA	
E.coli	:	TGTAAACACCCTAACCCGTGAAATCAAAAAACTCGA	
Sal	:	TGTGCAAACCGGGACCCGAGAAAATCAAAAAACTGGA	

Staph	:	TGGCGCTCTGGAACCTTCAGAGCTGGACTACGGGAAA	
E.coli	:	CGGCCGCTGTGCCCATTCAGTCGGATCGCGAAACTG	
Sal	:	CGGCCGCTGTGGTCGTTTGTATGGATAAGCGAAGACTG	

Staph	:	-GGACTCGAACAGAACAGTGGTACGAAAGCAAGCTGAC	
E.coli	:	TGGAAATTCTATCAGCGTTCTGTGGAAAGCGCGTTACA	
Sal	:	CGCCAACCGCGCAGCAATGGTGGCGTCAACCGTTACCG	

Staph	:	CGACACTATTACTATGGCCGTCCAAAGCACCTTACAA	
E.coli	:	AGAAAGCCGGGCAATTGCTGTGCCAGGCAGTTATAA	
Sal	:	CCAAAGCCGCGCTATCGCCGTTCGGGAAGCTATAA	

Staph	:	TGACATTGGCGTGACCAAGGAATCCGCAACCATAT	
E.coli	:	CGATCAGTTCCCGCATGGAGATATTCGTAAATTATGC	
Sal	:	CGATCAGTTGGCGGTGGCGAGATCCGCAATTATGT	

Staph	:	CGGATAATGTCTGGTACGAACGTGAGTCACGGTGGC	
E.coli	:	GGGCAACGTCTGGTATCAGCGCGAAGTCTTATACCC	
Sal	:	TGGCAACGTCTGGTATCAGCGTGAGATACGCAATCCC	

Staph	:	GGCCTATCTGAAGGATCAGCGTATGGTGCTCCGCTT	
E.coli	:	GAAAGGTTGGCAGGGCCAGCGTATCGTGCTGCGTT	
Sal	:	GAAAGGCTGGATCGCCAGCGCAAGTGTGCTGCGCTT	

FIG. 19A

Staph	:	CGGCTCTGCAACTCACAAAGCAATTGTCTATGTCAA	: 09/936759
E.coli	:	CGATGCCGTCACTCAATTACGGAAAGTGTGGTCAA	: 324
Sal	:	TGATGCCGTCACTCAATTACGGAAAGTGTGGTCAA	: 299
Staph	:	TGGTGAGCTGGTCGTGGAGCACAAAGGGGGATTCCT	: 347
E.coli	:	TAATCAGGAAGTGTGGAGCATCAGGGCGGTATAAC	: 360
Sal	:	TGACCAATTTTAATGGAACATGAGGGCGGTACAC	: 335
Staph	:	GCCATTGAAAGCGGAAATCAACAGCGCTGGCTGA	: 383
E.coli	:	GCCATTGAAAGCGGATGTCACGGCGTATGTTATGCG	: 396
Sal	:	GCCGTTGAAAGCGGATATCAGGCAGCTATCTCCSC	: 371
Staph	:	TGGCATGAAT--CGCGTCACGGTCCGGTGGACAA	: 416
E.coli	:	GGGGAAAAAGTGTACGGTACCGGTTCTGTGAACAA	: 432
Sal	:	GGGGAAATCCGTGGTACCGGTAACGGTGAATAA	: 407
Staph	:	CATCCTCGACGATAGCACCCCTCCCCGTGGCTGTA	: 452
E.coli	:	CGAACTGAACTGGCAGACATATCCCCGGGGAAATCG	: 467
Sal	:	CGAGCTGAACTGGCAGACGATCCCCGGGGCGT-TG	: 442
Staph	:	CAGCGAGGCCACGAAGAGGGCCCGGAAAGTCAT	: 488
E.coli	:	TGATTAACCGACGAAAACGG-----CAAGAAAAGCAG	: 499
Sal	:	TGACCCAGGGCGTAAACGG-----TAAGAACGCAA	: 474
Staph	:	TCTGAAACAAGCCGAACCTTGGACTTCTTCAACTATGC	: 524
E.coli	:	TCTTACTT-----CGATGAATTCTTAACTATGC	: 528
Sal	:	GCGTATTT-----CCATGATTCTTAACTACGC	: 503
Staph	:	AGGCCCTGCACCGTCCGGTGCAAAATCTACACGACCCC	: 560
E.coli	:	CGGGATCCATCGCAGCGTAATGGCTACACCAACGCC	: 564
Sal	:	CGGTATTCTACCGCAGCGTAATGGCTACACCAACGCC	: 539

FIG. 19B

Staph	:	GTTTACGTACGTGGAGGACATCTCGGTGTGACCGA	: 09/936759
E.coli	:	GAACACCTCTGGGTGGACGATATCACCGTCGTGACCGA	: 600
Sal	:	GAAACTTTGTGGAGATAATTACCGTCGTGACCGA	: 575
Staph	:	CTTCAATGCCCAACCGGGACTGTGACCTATAAGGT	: 632
E.coli	:	TGTGGGGAA--GACTSTAACCACGGGTCTGTGAG	: 634
Sal	:	GGTCTCTGAG--GATGTGGCTCAGGGTACCCGGG	: 609
Staph	:	GGAGTTCTAGGCAAAGCCGAGACCGTCAAAGTGTC	: 668
E.coli	:	TCGGCAGGTCTGTGGCCAAATGGTGAT-GTCAGGGITGA	: 669
Sal	:	GGCAGGTACGGGCGAAATGCCGAA-GTGCCTGTAGA	: 644
Staph	:	GGTCGTGGATGAGGAAGGCAAAGTGGTGGCAAGCAC	: 704
E.coli	:	ACTGGGTGATGGGGATCAACAGGTGGTGGCAAGTGG	: 705
Sal	:	GCTACGGTGAAGGGGAGCAACAGCTTGTCCTTGGG	: 680
Staph	:	CGAGGGCCTGAGCGGTAAACGGGAGATTCCGAAATGT	: 740
E.coli	:	ACAAGGGCACTAGCGGGACTTGGCAAGTGGTAAATCC	: 741
Sal	:	CGAAGGGGAAAAGCTGAAACGGTGTGGAAAGGGCC	: 716
Staph	:	CATCCTCTGGCAACCACTGAAACACCTATCTCTACCA	: 776
E.coli	:	GCACCTCTGGCAACCGGGTGAAGGTATCTCTAT--	: 775
Sal	:	GGGGCTCTGGCACCCCTGGCAGGGCTATCTTAT--	: 750
Staph	:	GATCAAAGTGGAACTGGTGAAGGACCGACTGACCAT	: 812
E.coli	:	GAACTGTGGCTCACACCCAAAAGCCAGACAGAGTGT	: 811
Sal	:	GAACCTGGGTCTATGGCAGCATCAGGACGAGCAG	: 786
Staph	:	CGATGTCTATGAAGAGCCGTTCGGGCTGCGGACCGT	: 848
E.coli.	:	-GATATCTACCCGCTTCGGCTCGGCAATCCGTCACT	: 846
Sal	:	-GATGAATATCCGCTGGCGTCGGTATTCGGCTCGGT	: 821

FIG. 19C

Staph	:	GGAAAGTCAACGACGGCAAGTCCTCATCAACAACAA	:	884
E.coli	:	GGCAGTCAAGGGCGAACAGTCCTGATCAACCACAA	:	882
Sal	:	AGAAGTAAAAGGGGAGCAGTCCTGATCAACCATAA	:	857
Staph	:	ACCGTTCTAGTTCAAGGCCTTGGCAAACATGAGGA	:	920
E.coli	:	ACCGTTCTACTTCACTGGCTTGGTCGTCAATGAGGA	:	918
Sal	:	GCTTTCTATTTCACGGGTTGGACGTCAATGAGGA	:	893
Staph	:	CACTCCATCAACGGCGTGGTTAACGAACCGAG	:	956
E.coli	:	TGCCGACTTACGTGGCAAAGGATTGATAACGTGGT	:	954
Sal	:	TGCCGACTGGGGGTAAAGGTTTGATAACGTGGT	:	929
Staph	:	CAATGTGATGGATTTCATAATCCCTCAAATGGATGG	:	992
E.coli	:	GATGGTGCAGGACCAAGCATTAAATGGACTGGATTTGG	:	990
Sal	:	GATGGTGCAGGACCAAGCGCTTAATGGATGGATGG	:	965
Staph	:	CGCGAACACCTTCCGACCGCACACTATCCGTACCTC	:	1028
E.coli	:	GGCGAACCTCCGTACCGTACCTCGCATTAACCTTACGC	:	1026
Sal	:	TGCGAACCTTACCGTACCTCGCATTAACCTTATGC	:	1001
Staph	:	TGAAGAGTGATGCGTCTTCCGGATCGCGAGGGTCT	:	1064
E.coli	:	TGAAGAGATGCTCGACTGGCCAGATGAAACATGGCAT	:	1062
Sal	:	CGAAGAGATGCTCGACTGGCGGACGAAACATGGCAT	:	1037
Staph	:	CGTGGTGATCGACCGACACTCCGGCAGTTCGGCTGCA	:	1100
E.coli	:	CGTGGTGATGATCAAACCTGCTGCTGTCGGTTTAA	:	1098
Sal	:	CGTCACTATGATCAAACGGCGCGCTCGGATTCAA	:	1073
Staph	:	CCTGAACTTCATGGCCACCAACGGCACCTCGGGAAAGG	:	1136
E.coli	:	CCTCTCTTTAGGATTGGTTTCAAGCCGGAAACAA	:	1134
Sal	:	CCTGTCCTTAGGATTAGCTTGTGTCGGGAAAAA	:	1109

FIG. 19D

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Staph	:	-----CAGCGAGGGGTCACTACCTGGGAGAAGATCC	:	1169
E.coli	:	GGCGAAAGAACCTACAGCGAACAGGGAGTCACGG	:	1170
Sal	:	ACCCAAAGAGCTCACAGCGATGAGGCCGTGAACGA	:	1145
Staph	:	GACGTTGAGCAC-----CATCAAGACGTTCTCCGTGA	:	1202
E.coli	:	GGAAAACTCAGCAAGGGCACTTAGAGGGGATTAAAGA	:	1206
Sal	:	TGAAACCCAGGGGCGACGCTGGAGGCAATTAGGA	:	1181
Staph	:	ACTGGTGTCTGGTGAAGAACCACTCAAGCGTCGT	:	1238
E.coli	:	GCTGATAGCGCGTGAGAAAAACCAAGCCAAGCGTCGT	:	1242
Sal	:	GCTGATGCCCCGATAAGAACCAAGCCAAGCGTCGT	:	1217
Staph	:	GATGTGGAGCATCGCCAACGGAGGCGCGACTGAGGA	:	1274
E.coli	:	GATGTGGAGCTATCGCCAACGAACCGGATACCCGTCC	:	1278
Sal	:	GATGTGGAGCTATCGCCAACGAACCGGATACCCGCCC	:	1253
Staph	:	AGAGGGGGTAGGGAGTAGTTCAAGCCGTGGTGG	:	1310
E.coli	:	CCA-AGTGCACGGGAATAATTTCG-----CCACTGGGG	:	1311
Sal	:	GAACGGGGCGGGGAATACCTCGCTCCGCTGGCCA	:	1289
Staph	:	GCTGACCAAGGAACCTCGACCCACAGAAAGCGTCGGT	:	1346
E.coli	:	AGCAACCGCTAAACTCGACCC-----GACCGCTCCGAT	:	1344
Sal	:	GGCAACCGCGAACCTCGATCC-----TACACGTCCGAT	:	1322
Staph	:	CACGATCGTCTGTTGTCATGGCTACCCGGAGAC	:	1382
E.coli	:	CACCTGGCTCAATGTAATGTTCTGCCACGGCTCACAC	:	1380
Sal	:	AACCTGGCTGAACGTGATGTTCTGCCATCCGGAAAG	:	1358
Staph	:	GGAGAAAGTGGCGAACCTGATTGACGTCACTGCCCT	:	1418
E.coli	:	GGATACCATCAGGGATCTCTTTGATGTGCTGGCT	:	1416
Sal	:	GGAGACCCATTACCGATCTCTTTGATGTGCTGGCT	:	1394

FIG. 19E

Staph : CAA[CGCTATAACGGATGGTACTTCGATGCCGGTGA : 099936759
E.coli : GAACCGT[TAFFACGGATGGTATGTCCAAAGCGGGGA : 1456
Sal : GAACCGTAC[ACGGCTGGTATGTACAAAGCGGGGA : 1430

Staph : TCTCGAAGGGCCAAGTCCATCTCCGCCAGGAATT : 1490
E.coli : T[CTGGAAACGGCAAGAAAGTACTGGAAAAGAAGT : 1488
Sal : TCTGGAGAAGGCTGAGAAAGTGCTGGAG[AAGACGT : 1466

Staph : TCACGCCTGGAACAAGCGTTGCCAGGAAAGCCGAT : 1526
E.coli : TCTGGCCTGGCAAGAACAAACTCC---[TCAGCCGAT : 1521
Sal : TCTGGCCTGGDAGGACAAACTCC---[ACGCCCGAT : 1499

Staph : CAICATCACTGAGTACGGCCAGACACCCTTGCCGG : 1562
E.coli : TATCATCACCGAATA[CGGGCTGGATACCTTAGEGG : 1557
Sal : TATCATCACCGAATA[CGGGCTCGATACCCCTGGAGG : 1535

Staph : GTTTCACGGACATGATCAGTGTATGTTACCGAGGA : 1598
E.coli : GCGGCACTCAATGTACACGGACATGTGGAGTGANGA : 1593
Sal : CGGCAATTCCATGTACAAAGGATATGTGGAGGAAAGA : 1571

Staph : ATATCAAGTGGAGTACTACCAGGCGAACACCGTCGT : 1634
E.coli : G[ATCACTGTCGATGGCTGGATATGTATCACCCTGT : 1629
Sal : GTACCACTGCGCTGGCTGATATCTACCATCGCGT : 1607

Staph : GTTCGATGAGTTGAGAAC[TCGTGGG[GAGGCAAGC : 1670
E.coli : CTTIGATCGCGTCAGCGCGTCGTGGG[GAAACAGGT : 1665
Sal : GTTIGATCGCGTCAGCGCGTCGTGGG[GAGCAGGT : 1643

Staph : GTGGAAC[TCGCGGACTTCGGCAGCCTCAGGGCGT : 1706
E.coli : ATGGAATT[TCGCGGATTTGGCAGCTCGCAAGGCAT : 1701
Sal : ATGGAAC[TCGCGGACTTCGGCAGCTCGCAGGGCAT : 1679

FIG. 19F

Figure 19G

Staph	:	GATGCGCGTCCAAGGAACAAAGAACGGCGTGTTCAC	:	1742
E.coli	:	ATGCGCGTTGGCGTACAAGAACGGCATCTTCAC	:	1737
Sal	:	TATGCGCGTTGGCGGAAACAAAAAGGTATAATTCAC	:	1715
Staph	:	TCGAGACGGCAAGCCGAAGCTCGCCGGCACCGCTT	:	1778
E.coli	:	TCGGGACCGGAAACCGAAGTCGGCGGCTTTCTGCT	:	1773
Sal	:	CGGGGACAGAAAACAAAAATCGGGCGGCCCTCCTGCT	:	1751
Staph	:	TCGGAGCGCTGGACCAAACATTCCAGATTTCGGCTA	:	1814
E.coli	:	GCAAAAAACGCTGGACTGGCAT-----GAAGTTGGTGA	:	1806
Sal	:	GCAAAAAACGCTGGACCGGGCAT-----GGACTTGGCGT	:	1784
Staph	:	CAAGAAC-----	:	1821
E.coli	:	AAAACGGCAGCAGGGAGGCACAAATGAATCAACAA	:	1842
Sal	:	GAAGCCCCAGCAGGGAGATAAAATGA-----	:	1812
Staph	:	-----	:	-
E.coli	:	CTCTCCTGGCGCACCATCGTCGGCTACAGCCTCGGT	:	1878
Sal	:	-----	:	-
Staph	:	-----	:	-
E.coli	:	GACGTCGCCAATAACTTCGCGCTTCGCAATGGGGCG	:	1914
Sal	:	-----	:	-
Staph	:	-----	:	-
E.coli	:	CTCTTCCTGTTGAGTTACTACACCGACGTCGCTGGC	:	1950
Sal	:	-----	:	-
Staph	:	-----	:	-
E.coli	:	GTCGGTGCCGCTGCGGCGGGCACCATGCTG	:	1980
Sal	:	-----	:	-

FIG. 19G